

# Gabriele Berg

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2118641/publications.pdf>

Version: 2024-02-01

288  
papers

29,553  
citations

4960

84  
h-index

6654

156  
g-index

308  
all docs

308  
docs citations

308  
times ranked

20508  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phyllosphere-associated microbiota in built environment: Do they have the potential to antagonize human pathogens?. <i>Journal of Advanced Research</i> , 2023, 43, 109-121.	9.5	9
2	Enhanced survival of multi-species biofilms under stress is promoted by low-abundant but antimicrobial-resistant keystone species. <i>Journal of Hazardous Materials</i> , 2022, 422, 126836.	12.4	17
3	Evidence for host-microbiome co-evolution in apple. <i>New Phytologist</i> , 2022, 234, 2088-2100.	7.3	40
4	Identification of Volatile Organic Compounds Emitted by Two Beneficial Endophytic <i>Pseudomonas</i> Strains from Olive Roots. <i>Plants</i> , 2022, 11, 318.	3.5	13
5	The emergence of disease-preventing bacteria within the plant microbiota. <i>Environmental Microbiology</i> , 2022, 24, 3259-3263.	3.8	14
6	The microbiome and resistome of apple fruits alter in the post-harvest period. <i>Environmental Microbiomes</i> , 2022, 17, 10.	5.0	11
7	The plant microbiota signature of the Anthropocene as a challenge for microbiome research. <i>Microbiome</i> , 2022, 10, 54.	11.1	32
8	Exploring microbiomes for plant disease management. <i>Biological Control</i> , 2022, 169, 104890.	3.0	10
9	Insights into the microbiome assembly during different growth stages and storage of strawberry plants. <i>Environmental Microbiomes</i> , 2022, 17, 21.	5.0	18
10	The <i>Brassica napus</i> seed microbiota is cultivar-specific and transmitted via paternal breeding lines. <i>Microbial Biotechnology</i> , 2022, 15, 2379-2390.	4.2	14
11	<i>Fusarium</i> fruiting body microbiome member <i>Pantoea agglomerans</i> inhibits fungal pathogenesis by targeting lipid rafts. <i>Nature Microbiology</i> , 2022, 7, 831-843.	13.3	44
12	Bacterial-fungal interactions under agricultural settings: from physical to chemical interactions. <i>Stress Biology</i> , 2022, 2, .	3.1	7
13	Recovery of metagenome-assembled genomes from the phyllosphere of 110 rice genotypes. <i>Scientific Data</i> , 2022, 9, .	5.3	5
14	Metadata harmonization- Standards are the key for a better usage of omics data for integrative microbiome analysis. <i>Environmental Microbiomes</i> , 2022, 17, .	5.0	13
15	Bacterial communities in the plant phyllosphere harbour distinct responders to a broad-spectrum pesticide. <i>Science of the Total Environment</i> , 2021, 751, 141799.	8.0	46
16	Plant resistome profiling in evolutionary old bog vegetation provides new clues to understand emergence of multi-resistance. <i>ISME Journal</i> , 2021, 15, 921-937.	9.8	33
17	Towards a unified data infrastructure to support European and global microbiome research: a call to action. <i>Environmental Microbiology</i> , 2021, 23, 372-375.	3.8	7
18	The Himalayan Onion ( <i>Allium wallichii</i> Kunth) Harbors Unique Spatially Organized Bacterial Communities. <i>Microbial Ecology</i> , 2021, 82, 909-918.	2.8	8

#	ARTICLE	IF	CITATIONS
19	Identification of new eligible indicator organisms for combined sewer overflow via 16S rRNA gene amplicon sequencing in Kanda River, Tokyo. <i>Journal of Environmental Management</i> , 2021, 284, 112059.	7.8	10
20	Microbiome-Assisted Breeding to Understand Cultivar-Dependent Assembly in <i>Cucurbita pepo</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 642027.	3.6	24
21	Microbiome Modulation—Toward a Better Understanding of Plant Microbiome Response to Microbial Inoculants. <i>Frontiers in Microbiology</i> , 2021, 12, 650610.	3.5	78
22	Global analysis of the apple fruit microbiome: are all apples the same?. <i>Environmental Microbiology</i> , 2021, 23, 6038-6055.	3.8	64
23	Post-translational regulation of autophagy is involved in intra-microbiome suppression of fungal pathogens. <i>Microbiome</i> , 2021, 9, 131.	11.1	36
24	Occurrence of green mold disease on <i>Dictyophora rubrovolvata</i> caused by <i>Trichoderma koningiopsis</i> . <i>Journal of Plant Pathology</i> , 2021, 103, 981-984.	1.2	14
25	Bog ecosystems as a playground for plant–microbe coevolution: bryophytes and vascular plants harbour functionally adapted bacteria. <i>Microbiome</i> , 2021, 9, 170.	11.1	28
26	Explorative assessment of coronavirus-like short sequences from host-associated and environmental metagenomes. <i>Science of the Total Environment</i> , 2021, 793, 148494.	8.0	0
27	Plant Health and Sound Vibration: Analyzing Implications of the Microbiome in Grape Wine Leaves. <i>Pathogens</i> , 2021, 10, 63.	2.8	13
28	Antimicrobial-specific response from resistance gene carriers studied in a natural, highly diverse microbiome. <i>Microbiome</i> , 2021, 9, 29.	11.1	13
29	Bacterial seed endophyte shapes disease resistance in rice. <i>Nature Plants</i> , 2021, 7, 60-72.	9.3	220
30	Studying Seed Microbiomes. <i>Methods in Molecular Biology</i> , 2021, 2232, 1-21.	0.9	5
31	Fusaricidins, Polymyxins and Volatiles Produced by <i>Paenibacillus polymyxa</i> Strains DSM 32871 and M1. <i>Pathogens</i> , 2021, 10, 1485.	2.8	14
32	Increased Yield and High Resilience of Microbiota Representatives With Organic Soil Amendments in Smallholder Farms of Uganda. <i>Frontiers in Plant Science</i> , 2021, 12, 815377.	3.6	0
33	Microbiome-Guided Exploration of the Microbial Assemblage of the Exotic Beverage “Insect Tea” Native to Southwestern China. <i>Frontiers in Microbiology</i> , 2020, 10, 3087.	3.5	2
34	Assembly of Bacterial Genomes from the Metagenomes of Three Lichen Species. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
35	Reconstruction of Bacterial Metagenome-Assembled Genome Sequences from Alpine Bog Vegetation. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
36	Trichomes form genotype-specific microbial hotspots in the phyllosphere of tomato. <i>Environmental Microbiomes</i> , 2020, 15, 17.	5.0	14

#	ARTICLE	IF	CITATIONS
37	Conventional seed coating reduces prevalence of proteobacterial endophytes in <i>Nicotiana tabacum</i> . <i>Industrial Crops and Products</i> , 2020, 155, 112784.	5.2	16
38	Verticillium Wilt in Oilseed Rape—the Microbiome is Crucial for Disease Outbreaks as Well as for Efficient Suppression. <i>Plants</i> , 2020, 9, 866.	3.5	6
39	Exploring the Microbiota of East African Indigenous Leafy Greens for Plant Growth, Health, and Resilience. <i>Frontiers in Microbiology</i> , 2020, 11, 585690.	3.5	5
40	Understanding the Impact of Cultivar, Seed Origin, and Substrate on Bacterial Diversity of the Sugar Beet Rhizosphere and Suppression of Soil-Borne Pathogens. <i>Frontiers in Plant Science</i> , 2020, 11, 560869.	3.6	27
41	Microbiome Management by Biological and Chemical Treatments in Maize Is Linked to Plant Health. <i>Microorganisms</i> , 2020, 8, 1506.	3.6	17
42	A New High-Throughput Screening Method to Detect Antimicrobial Volatiles from Metagenomic Clone Libraries. <i>Antibiotics</i> , 2020, 9, 726.	3.7	2
43	Archaea, tiny helpers of land plants. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2494-2500.	4.1	35
44	The microbiome of alpine snow algae shows a specific inter-kingdom connectivity and algae-bacteria interactions with supportive capacities. <i>ISME Journal</i> , 2020, 14, 2197-2210.	9.8	46
45	Unraveling the Complexity of Soil Microbiomes in a Large-Scale Study Subjected to Different Agricultural Management in Styria. <i>Frontiers in Microbiology</i> , 2020, 11, 1052.	3.5	32
46	Microbiome approaches provide the key to biologically control postharvest pathogens and storability of fruits and vegetables. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	54
47	Plant Growth-Promoting Methylobacteria Selectively Increase the Biomass of Biotechnologically Relevant Microalgae. <i>Frontiers in Microbiology</i> , 2020, 11, 427.	3.5	26
48	Microbiome definition re-visited: old concepts and new challenges. <i>Microbiome</i> , 2020, 8, 103.	11.1	903
49	Profiling for Bioactive Peptides and Volatiles of Plant Growth Promoting Strains of the <i>Bacillus subtilis</i> Complex of Industrial Relevance. <i>Frontiers in Microbiology</i> , 2020, 11, 1432.	3.5	22
50	Microbiome-guided evaluation of <i>Bacillus subtilis</i> BIOUFLA2 application to reduce mycotoxins in maize kernels. <i>Biological Control</i> , 2020, 150, 104370.	3.0	10
51	<i>Nicotiana tabacum</i> seed endophytic communities share a common core structure and genotype-specific signatures in diverging cultivars. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 287-295.	4.1	35
52	Tomato-Associated Archaea Show a Cultivar-Specific Rhizosphere Effect but an Unspecific Transmission by Seeds. <i>Phytobiomes Journal</i> , 2020, 4, 133-141.	2.7	31
53	Insights into the community structure and lifestyle of the fungal root endophytes of tomato by combining amplicon sequencing and isolation approaches with phytohormone profiling. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	31
54	How Microbiome Approaches Can Assist Industrial Development of Biological Control Products. <i>Progress in Biological Control</i> , 2020, , 201-215.	0.5	5

#	ARTICLE	IF	CITATIONS
55	Volatile Interplay Between Microbes: Friends and Foes. , 2020, , 215-235.		4
56	Using Bacteria-Derived Volatile Organic Compounds (VOCs) for Industrial Processes. , 2020, , 305-316.		2
57	P450 <sub>hcb</sub> : A New, Robust and $\alpha$ -Selective Fatty Acid Hydroxylase Displaying Unexpected $\alpha$ -Alkene Formation. Chemistry - A European Journal, 2020, 26, 15910-15921.	3.3	8
58	Microbiome-driven identification of microbial indicators for postharvest diseases of sugar beets. Microbiome, 2019, 7, 112.	11.1	68
59	An Apple a Day: Which Bacteria Do We Eat With Organic and Conventional Apples?. Frontiers in Microbiology, 2019, 10, 1629.	3.5	87
60	Revealing Cues for Fungal Interplay in the Plant-Air Interface in Vineyards. Frontiers in Plant Science, 2019, 10, 922.	3.6	36
61	Seeds of native alpine plants host unique microbial communities embedded in cross-kingdom networks. Microbiome, 2019, 7, 108.	11.1	87
62	Microbiome Response to Hot Water Treatment and Potential Synergy With Biological Control on Stored Apples. Frontiers in Microbiology, 2019, 10, 2502.	3.5	50
63	The Role of Volatile Organic Compounds and Rhizosphere Competence in Mode of Action of the Non-pathogenic Fusarium oxysporum FO12 Toward Verticillium Wilt. Frontiers in Microbiology, 2019, 10, 1808.	3.5	27
64	Deciphering the microbiome shift during fermentation of medicinal plants. Scientific Reports, 2019, 9, 13461.	3.3	12
65	Enterobacteriaceae dominate the core microbiome and contribute to the resistome of arugula (Eruca) Tj ETQq1 1 0,784314 rgBT /Overd	11.1	84
66	Novel Strategies for Soil-Borne Diseases: Exploiting the Microbiome and Volatile-Based Mechanisms Toward Controlling Meloidogyne-Based Disease Complexes. Frontiers in Microbiology, 2019, 10, 1296.	3.5	60
67	Microbiota Associated with Sclerotia of Soilborne Fungal Pathogens $\alpha$ A Novel Source of Biocontrol Agents Producing Bioactive Volatiles. Phytobiomes Journal, 2019, 3, 125-136.	2.7	41
68	Novel insights into plant-associated archaea and their functioning in arugula (Eruca sativa Mill.). Journal of Advanced Research, 2019, 19, 39-48.	9.5	49
69	A novel, nature-based alternative for photobioreactor decontaminations. Scientific Reports, 2019, 9, 2864.	3.3	14
70	Disease Incidence in Sugar Beet Fields Is Correlated with Microbial Diversity and Distinct Biological Markers. Phytobiomes Journal, 2019, 3, 22-30.	2.7	47
71	Understanding the Indigenous Seed Microbiota to Design Bacterial Seed Treatments. , 2019, , 83-99.		10
72	Man-made microbial resistances in built environments. Nature Communications, 2019, 10, 968.	12.8	128

#	ARTICLE	IF	CITATIONS
73	The tea leaf microbiome shows specific responses to chemical pesticides and biocontrol applications. <i>Science of the Total Environment</i> , 2019, 667, 33-40.	8.0	47
74	Plasticity of a holobiont: desiccation induces fasting-like metabolism within the lichen microbiota. <i>ISME Journal</i> , 2019, 13, 547-556.	9.8	37
75	Endophytic Fungi of Native <i>Salvia abrotanoides</i> Plants Reveal High Taxonomic Diversity and Unique Profiles of Secondary Metabolites. <i>Frontiers in Microbiology</i> , 2019, 10, 3013.	3.5	40
76	What are the organismic elements of vegetation science?. <i>Applied Vegetation Science</i> , 2018, 21, 341-344.	1.9	5
77	The impact of human activities and lifestyles on the interlinked microbiota and health of humans and of ecosystems. <i>Science of the Total Environment</i> , 2018, 627, 1018-1038.	8.0	244
78	Saving seed microbiomes. <i>ISME Journal</i> , 2018, 12, 1167-1170.	9.8	211
79	First evaluation of alkylpyrazine application as a novel method to decrease microbial contaminations in processed meat products. <i>AMB Express</i> , 2018, 8, 54.	3.0	17
80	Biocontrol of plant diseases is not an unsafe technology!. <i>Journal of Plant Diseases and Protection</i> , 2018, 125, 121-125.	2.9	31
81	The <i>Cucurbita pepo</i> seed microbiome: genotype-specific composition and implications for breeding. <i>Plant and Soil</i> , 2018, 422, 35-49.	3.7	131
82	Archaea Are Interactive Components of Complex Microbiomes. <i>Trends in Microbiology</i> , 2018, 26, 70-85.	7.7	203
83	Enriching Beneficial Microbial Diversity of Indoor Plants and Their Surrounding Built Environment With Biostimulants. <i>Frontiers in Microbiology</i> , 2018, 9, 2985.	3.5	25
84	Adaptions of Lichen Microbiota Functioning Under Persistent Exposure to Arsenic Contamination. <i>Frontiers in Microbiology</i> , 2018, 9, 2959.	3.5	16
85	Tomato Seeds Preferably Transmit Plant Beneficial Endophytes. <i>Phytobiomes Journal</i> , 2018, 2, 183-193.	2.7	124
86	Leaves of Indoor Ornamentals Are Biodiversity and Functional Hotspots for Fungi. <i>Frontiers in Microbiology</i> , 2018, 9, 2343.	3.5	9
87	<i>Stenotrophomonas maltophilia</i> . <i>Trends in Microbiology</i> , 2018, 26, 637-638.	7.7	83
88	What Is the Role of <i>Archaea</i> in Plants? New Insights from the Vegetation of Alpine Bogs. <i>MSphere</i> , 2018, 3, .	2.9	78
89	Ecotype-Dependent Response of Bacterial Communities Associated with <i>Arabidopsis</i> to Cold Acclimation. <i>Phytobiomes Journal</i> , 2018, 2, 3-13.	2.7	8
90	Differential sharing and distinct co-occurrence networks among spatially close bacterial microbiota of bark, mosses and lichens. <i>Molecular Ecology</i> , 2017, 26, 2826-2838.	3.9	79

#	ARTICLE	IF	CITATIONS
91	Decision-Making and Credition Under a Microbial Perspective. New Approaches To the Scientific Study of Religion, 2017, , 443-450.	0.3	4
92	Plant microbial diversity is suggested as the key to future biocontrol and health trends. FEMS Microbiology Ecology, 2017, 93, .	2.7	376
93	Members of Gammaproteobacteria as indicator species of healthy banana plants on Fusarium wilt-infested fields in Central America. Scientific Reports, 2017, 7, 45318.	3.3	89
94	Symbiotic Interplay of Fungi, Algae, and Bacteria within the Lung Lichen <i>Lobaria pulmonaria</i> L. Hoffm. as Assessed by State-of-the-Art Metaproteomics. Journal of Proteome Research, 2017, 16, 2160-2173.	3.7	43
95	Discovery of Polyesterases from Moss-Associated Microorganisms. Applied and Environmental Microbiology, 2017, 83, .	3.1	29
96	Replacing conventional decontamination of hatching eggs with a natural defense strategy based on antimicrobial, volatile pyrazines. Scientific Reports, 2017, 7, 13253.	3.3	27
97	Complete genome sequence of <i>Pseudomonas brassicacearum</i> strain L13-6-12, a biological control agent from the rhizosphere of potato. Standards in Genomic Sciences, 2017, 12, 6.	1.5	19
98	Harnessing the microbiomes of Brassica vegetables for health issues. Scientific Reports, 2017, 7, 17649.	3.3	47
99	Preparing for the crewed Mars journey: microbiota dynamics in the confined Mars500 habitat during simulated Mars flight and landing. Microbiome, 2017, 5, 129.	11.1	47
100	Aerial Warfare: A Volatile Dialogue between the Plant Pathogen <i>Verticillium longisporum</i> and Its Antagonist <i>Paenibacillus polymyxa</i> . Frontiers in Plant Science, 2017, 8, 1294.	3.6	78
101	Editorial: A Multidisciplinary Look at <i>Stenotrophomonas maltophilia</i> : An Emerging Multi-Drug-Resistant Global Opportunistic Pathogen. Frontiers in Microbiology, 2017, 8, 1511.	3.5	58
102	Antimicrobial Activity of Medicinal Plants Correlates with the Proportion of Antagonistic Endophytes. Frontiers in Microbiology, 2017, 8, 199.	3.5	136
103	Double-Face Meets the Bacterial World: The Opportunistic Pathogen <i>Stenotrophomonas maltophilia</i> . Frontiers in Microbiology, 2017, 8, 2190.	3.5	66
104	Deciphering functional diversification within the lichen microbiota by meta-omics. Microbiome, 2017, 5, 82.	11.1	91
105	The structure of the Brassica napus seed microbiome is cultivar-dependent and affects the interactions of symbionts and pathogens. Microbiome, 2017, 5, 104.	11.1	144
106	Complete genome sequence of <i>Pseudomonas corrugata</i> strain RM1-1-4, a stress protecting agent from the rhizosphere of an oilseed rape bait plant. Standards in Genomic Sciences, 2017, 12, 66.	1.5	4
107	Understanding Microbial Multi-Species Symbioses. Frontiers in Microbiology, 2016, 7, 180.	3.5	140
108	Biochar Treatment Resulted in a Combined Effect on Soybean Growth Promotion and a Shift in Plant Growth Promoting Rhizobacteria. Frontiers in Microbiology, 2016, 7, 209.	3.5	114

#	ARTICLE	IF	CITATIONS
109	Biological Control of Lettuce Drop and Host Plant Colonization by Rhizospheric and Endophytic Streptomyces. <i>Frontiers in Microbiology</i> , 2016, 7, 714.	3.5	51
110	Controlling the Microbiome: Microhabitat Adjustments for Successful Biocontrol Strategies in Soil and Human Gut. <i>Frontiers in Microbiology</i> , 2016, 7, 1079.	3.5	37
111	Microorganisms in Confined Habitats: Microbial Monitoring and Control of Intensive Care Units, Operating Rooms, Cleanrooms and the International Space Station. <i>Frontiers in Microbiology</i> , 2016, 7, 1573.	3.5	106
112	Endemic plants harbour specific Trichoderma communities with an exceptional potential for biocontrol of phytopathogens. <i>Journal of Biotechnology</i> , 2016, 235, 162-170.	3.8	37
113	Comparisons of diazotrophic communities in native and agricultural desert ecosystems reveal plants as important drivers in diversity. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv166.	2.7	37
114	High Life Expectancy of Bacteria on Lichens. <i>Microbial Ecology</i> , 2016, 72, 510-513.	2.8	17
115	The plant is crucial: specific composition and function of the phyllosphere microbiome of indoor ornamentals. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw173.	2.7	41
116	Complete genome sequences of the <i>Serratia plymuthica</i> strains 3Rp8 and 3Re4-18, two rhizosphere bacteria with antagonistic activity towards fungal phytopathogens and plant growth promoting abilities. <i>Standards in Genomic Sciences</i> , 2016, 11, 61.	1.5	20
117	Lichens as natural sources of biotechnologically relevant bacteria. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 583-595.	3.6	48
118	9 Lichen-Bacterial Interactions. , 2016, , 179-188.		5
119	Bioprospecting plant-associated microbiomes. <i>Journal of Biotechnology</i> , 2016, 235, 171-180.	3.8	53
120	The plant microbiome explored: implications for experimental botany. <i>Journal of Experimental Botany</i> , 2016, 67, 995-1002.	4.8	424
121	Synergistic interactions between <i>Bradyrhizobium japonicum</i> and the endophyte <i>Stenotrophomonas rhizophila</i> and their effects on growth, and nodulation of soybean under salt stress. <i>Plant and Soil</i> , 2016, 405, 35-45.	3.7	116
122	Kill or cure? The interaction between endophytic <i>Paenibacillus</i> and <i>Serratia</i> strains and the host plant is shaped by plant growth conditions. <i>Plant and Soil</i> , 2016, 405, 65-79.	3.7	37
123	Endophytes-assisted biocontrol: novel insights in ecology and the mode of action of <i>Paenibacillus</i> . <i>Plant and Soil</i> , 2016, 405, 125-140.	3.7	150
124	Mycobiome in the Lower Respiratory Tract – A Clinical Perspective. <i>Frontiers in Microbiology</i> , 2016, 07, 2169.	3.5	36
125	The <i>Flavobacterium</i> Genus in the Plant Holobiont: Ecological, Physiological, and Applicative Insights. , 2016, , 189-207.		37
126	The Novel Lipopeptide Poaeamide of the Endophyte <i>Pseudomonas poae</i> RE*1-1-14 Is Involved in Pathogen Suppression and Root Colonization. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 800-810.	2.6	105



#	ARTICLE	IF	CITATIONS
127	Transgenic banana plants expressing <i>Xanthomonas</i> wilt resistance genes revealed a stable non-target bacterial colonization structure. <i>Scientific Reports</i> , 2015, 5, 18078.	3.3	31
128	The core microbiome bonds the Alpine bog vegetation to a transkingdom metacommunity. <i>Molecular Ecology</i> , 2015, 24, 4795-4807.	3.9	74
129	A novel assay for the detection of bioactive volatiles evaluated by screening of lichen-associated bacteria. <i>Frontiers in Microbiology</i> , 2015, 6, 398.	3.5	85
130	Analyzing the antagonistic potential of the lichen microbiome against pathogens by bridging metagenomic with culture studies. <i>Frontiers in Microbiology</i> , 2015, 6, 620.	3.5	65
131	Microbiome interplay: plants alter microbial abundance and diversity within the built environment. <i>Frontiers in Microbiology</i> , 2015, 6, 887.	3.5	62
132	Cross-Kingdom Similarities in Microbiome Ecology and Biocontrol of Pathogens. <i>Frontiers in Microbiology</i> , 2015, 6, 1311.	3.5	24
133	Biotic Stress Shifted Structure and Abundance of Enterobacteriaceae in the Lettuce Microbiome. <i>PLoS ONE</i> , 2015, 10, e0118068.	2.5	51
134	Cleanroom Maintenance Significantly Reduces Abundance but Not Diversity of Indoor Microbiomes. <i>PLoS ONE</i> , 2015, 10, e0134848.	2.5	56
135	Beyond borders: investigating microbiome interactivity and diversity for advanced biocontrol technologies. <i>Microbial Biotechnology</i> , 2015, 8, 5-7.	4.2	33
136	Mining for Nonribosomal Peptide Synthetase and Polyketide Synthase Genes Revealed a High Level of Diversity in the Sphagnum Bog Metagenome. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5064-5072.	3.1	29
137	Complete Genome Sequence of <i>Paenibacillus polymyxa</i> Strain Sb3-1, a Soilborne Bacterium with Antagonistic Activity toward Plant Pathogens. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
138	Draft Genome Sequence of <i>Streptomyces</i> sp. Strain Wb2n-11, a Desert Isolate with Broad-Spectrum Antagonism against Soilborne Phytopathogens. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
139	Complete Genome Sequence of <i>Bacillus amyloliquefaciens</i> Strain Co1-6, a Plant Growth-Promoting Rhizobacterium of <i>Calendula officinalis</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	2
140	Plant-Microbe Interactions and Water Management in Arid and Saline Soils. , 2015, , 265-276.		20
141	The Edible Plant Microbiome: Importance and Health Issues. , 2015, , 419-426.		19
142	Agroforestry leads to shifts within the gammaproteobacterial microbiome of banana plants cultivated in Central America. <i>Frontiers in Microbiology</i> , 2015, 6, 91.	3.5	40
143	Plant genotype-specific archaeal and bacterial endophytes but similar <i>Bacillus</i> antagonists colonize Mediterranean olive trees. <i>Frontiers in Microbiology</i> , 2015, 6, 138.	3.5	154
144	The Hidden World within Plants: Ecological and Evolutionary Considerations for Defining Functioning of Microbial Endophytes. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 293-320.	6.6	1,895

#	ARTICLE	IF	CITATIONS
145	Friends or foes: can we make a distinction between beneficial and harmful strains of the <i>Stenotrophomonas maltophilia</i> complex?. <i>Frontiers in Microbiology</i> , 2015, 6, 241.	3.5	95
146	Rhizobiales as functional and endosymbiotic members in the lichen symbiosis of <i>Lobaria pulmonaria</i> L.. <i>Frontiers in Microbiology</i> , 2015, 6, 53.	3.5	196
147	Visualization of Plant-Microbe Interactions. , 2015, , 299-306.		8
148	Quo vadis? Microbial profiling revealed strong effects of cleanroom maintenance and routes of contamination in indoor environments. <i>Scientific Reports</i> , 2015, 5, 9156.	3.3	52
149	Draft Genome Sequence of <i>Paenibacillus polymyxa</i> Strain Mc5Re-14, an Antagonistic Root Endophyte of <i>Matricaria chamomilla</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	4
150	Bacterial networks and co-occurrence relationships in the lettuce root microbiota. <i>Environmental Microbiology</i> , 2015, 17, 239-252.	3.8	241
151	Exploring functional contexts of symbiotic sustain within lichen-associated bacteria by comparative omics. <i>ISME Journal</i> , 2015, 9, 412-424.	9.8	238
152	Beneficial effects of plant-associated microbes on indoor microbiomes and human health?. <i>Frontiers in Microbiology</i> , 2014, 5, 15.	3.5	74
153	The impact of the pathogen <i>Rhizoctonia solani</i> and its beneficial counterpart <i>Bacillus amyloliquefaciens</i> on the indigenous lettuce microbiome. <i>Frontiers in Microbiology</i> , 2014, 5, 175.	3.5	141
154	Vegetable microbiomes: is there a connection among opportunistic infections, human health and our 'gut feeling'?. <i>Microbial Biotechnology</i> , 2014, 7, 487-495.	4.2	75
155	Microbial cargo: do bacteria on symbiotic propagules reinforce the microbiome of lichens?. <i>Environmental Microbiology</i> , 2014, 16, 3743-3752.	3.8	78
156	Unraveling the plant microbiome: looking back and future perspectives. <i>Frontiers in Microbiology</i> , 2014, 5, 148.	3.5	498
157	The plant microbiome and its importance for plant and human health. <i>Frontiers in Microbiology</i> , 2014, 5, 491.	3.5	128
158	Differences between the rhizosphere microbiome of <i>Beta vulgaris</i> ssp. <i>maritima</i> ancestor of all beet crops and modern sugar beets. <i>Frontiers in Microbiology</i> , 2014, 5, 415.	3.5	124
159	Effects of sample handling and cultivation bias on the specificity of bacterial communities in keratose marine sponges. <i>Frontiers in Microbiology</i> , 2014, 5, 611.	3.5	39
160	Effects of bacterial inoculants on the indigenous microbiome and secondary metabolites of chamomile plants. <i>Frontiers in Microbiology</i> , 2014, 5, 64.	3.5	123
161	The <i>Sphagnum</i> microbiome supports bog ecosystem functioning under extreme conditions. <i>Molecular Ecology</i> , 2014, 23, 4498-4510.	3.9	98
162	<i>Stenotrophomonas</i> comparative genomics reveals genes and functions that differentiate beneficial and pathogenic bacteria. <i>BMC Genomics</i> , 2014, 15, 482.	2.8	90

#	ARTICLE	IF	CITATIONS
163	A Function of SmeDEF, the Major Quinolone Resistance Determinant of <i>Stenotrophomonas maltophilia</i> , Is the Colonization of Plant Roots. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4559-4565.	3.1	75
164	Understanding the Diversity and Versatility of Trichoderma by Next-Generation Sequencing. , 2014, , 57-65.		2
165	Endophytic bacteria of Sphagnum mosses as promising objects of agricultural microbiology. <i>Microbiology</i> , 2013, 82, 306-315.	1.2	59
166	The ignored diversity: complex bacterial communities in intensive care units revealed by 16S pyrosequencing. <i>Scientific Reports</i> , 2013, 3, 1413.	3.3	148
167	<i>Bacillus</i> and <i>Streptomyces</i> were selected as broad-spectrum antagonists against soilborne pathogens from arid areas in Egypt. <i>FEMS Microbiology Letters</i> , 2013, 342, 168-178.	1.8	104
168	A study of the bacterial community in the root system of the maytansine containing plant <i>Putterlickia verrucosa</i> . <i>Phytochemistry</i> , 2013, 91, 158-164.	2.9	27
169	Localization of bacteria in lichens from Alpine soil crusts by fluorescence in situ hybridization. <i>Applied Soil Ecology</i> , 2013, 68, 20-25.	4.3	31
170	Alleviation of salt stress of symbiotic <i>Galega officinalis</i> L. (goat's rue) by co-inoculation of <i>Rhizobium</i> with root-colonizing <i>Pseudomonas</i> . <i>Plant and Soil</i> , 2013, 369, 453-465.	3.7	123
171	Insights into functional bacterial diversity and its effects on Alpine bog ecosystem functioning. <i>Scientific Reports</i> , 2013, 3, 1955.	3.3	71
172	Complete Genome Sequence of the Sugar Beet Endophyte <i>Pseudomonas poae</i> RE*1-1-14, a Disease-Suppressive Bacterium. <i>Genome Announcements</i> , 2013, 1, e0002013.	0.8	20
173	Genome Sequence of <i>Serratia plymuthica</i> Strain S13, an Endophyte with Germination- and Plant-Growth-Promoting Activity from the Flower of Styrian Oil Pumpkin. <i>Genome Announcements</i> , 2013, 1, .	0.8	13
174	Root-microbe systems: the effect and mode of interaction of Stress Protecting Agent (SPA) <i>Stenotrophomonas rhizophila</i> DSM14405T. <i>Frontiers in Plant Science</i> , 2013, 4, 141.	3.6	127
175	Real-time PCR assay to detect <i>Verticillium albo-atrum</i> and <i>V. dahliae</i> in hops: development and comparison with a standard PCR method. <i>Journal of Plant Diseases and Protection</i> , 2013, 120, 105-114.	2.9	17
176	Next-Generation Bio-Products Sowing the Seeds of Success for Sustainable Agriculture. <i>Agronomy</i> , 2013, 3, 648-656.	3.0	150
177	The DSF Quorum Sensing System Controls the Positive Influence of <i>Stenotrophomonas maltophilia</i> on Plants. <i>PLoS ONE</i> , 2013, 8, e67103.	2.5	51
178	Vertical transmission explains the specific Burkholderia pattern in Sphagnum mosses at multi-geographic scale. <i>Frontiers in Microbiology</i> , 2013, 4, 394.	3.5	43
179	Initial Steps towards Biocontrol in Hops: Successful Colonization and Plant Growth Promotion by Four Bacterial Biocontrol Agents. <i>Agronomy</i> , 2013, 3, 583-594.	3.0	11
180	Catch the Best: Novel Screening Strategy to Select Stress Protecting Agents for Crop Plants. <i>Agronomy</i> , 2013, 3, 794-815.	3.0	38

#	ARTICLE	IF	CITATIONS
181	The microbiome of medicinal plants: diversity and importance for plant growth, quality and health. <i>Frontiers in Microbiology</i> , 2013, 4, 400.	3.5	224
182	Banana-Associated Microbial Communities in Uganda Are Highly Diverse but Dominated by Enterobacteriaceae. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4933-4941.	3.1	49
183	A new textile-based approach to assess the antimicrobial activity of volatiles. <i>Textile Research Journal</i> , 2012, 82, 484-491.	2.2	5
184	Trichoderma-Plant-Pathogen Interactions: Advances in Genetics of Biological Control. <i>Indian Journal of Microbiology</i> , 2012, 52, 522-529.	2.7	173
185	<i>Sphagnum</i> mosses harbour highly specific bacterial diversity during their whole lifecycle. <i>ISME Journal</i> , 2012, 6, 802-813.	9.8	161
186	Biocontrol of <i>Rhizoctonia solani</i> : complex interaction of biocontrol strains, pathogen and indigenous microbial community in the rhizosphere of lettuce shown by molecular methods. <i>Plant and Soil</i> , 2012, 361, 343-357.	3.7	47
187	Promotion of growth, health and stress tolerance of Styrian oil pumpkins by bacterial endophytes. <i>European Journal of Plant Pathology</i> , 2012, 134, 509-519.	1.7	46
188	<i>Stenotrophomonas rhizophila</i> DSM14405T promotes plant growth probably by altering fungal communities in the rhizosphere. <i>Biology and Fertility of Soils</i> , 2012, 48, 947-960.	4.3	72
189	Bacterial taxa associated with the lung lichen <i>Lobaria pulmonaria</i> are differentially shaped by geography and habitat. <i>FEMS Microbiology Letters</i> , 2012, 329, 111-115.	1.8	56
190	Age, sun and substrate: triggers of bacterial communities in lichens. <i>Environmental Microbiology Reports</i> , 2012, 4, 23-28.	2.4	74
191	Alphaproteobacterial communities in geographically distant populations of the lichen <i>Cetraria aculeata</i> . <i>FEMS Microbiology Ecology</i> , 2012, 82, 316-325.	2.7	50
192	Host-parasite interaction and microbiome response: effects of fungal infections on the bacterial community of the Alpine lichen <i>Solorina crocea</i> . <i>FEMS Microbiology Ecology</i> , 2012, 82, 472-481.	2.7	48
193	Microbial Diversity Inside Pumpkins: Microhabitat-Specific Communities Display a High Antagonistic Potential Against Phytopathogens. <i>Microbial Ecology</i> , 2012, 63, 418-428.	2.8	128
194	<i>Fronidhabitans cladoniiphilus</i> sp. nov., an actinobacterium of the family Microbacteriaceae isolated from lichen, and emended description of the genus <i>Fronidhabitans</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 3033-3038.	1.7	37
195	PGPR Interplay with Rhizosphere Communities and Effect on Plant Growth and Health. , 2011, , 97-109.		6
196	Impact of biotic and a-biotic parameters on structure and function of microbial communities living on sclerotia of the soil-borne pathogenic fungus <i>Rhizoctonia solani</i> . <i>Applied Soil Ecology</i> , 2011, 48, 193-200.	4.3	28
197	Black fungi and associated bacterial communities in the phyllosphere of grapevine. <i>Fungal Biology</i> , 2011, 115, 978-986.	2.5	67
198	Using Ecological Knowledge and Molecular Tools to Develop Effective and Safe Biocontrol Strategies. , 2011, , .		3

#	ARTICLE	IF	CITATIONS
199	Desert Farming Benefits from Microbial Potential in Arid Soils and Promotes Diversity and Plant Health. PLoS ONE, 2011, 6, e24452.	2.5	200
200	PhyloChip hybridization uncovered an enormous bacterial diversity in the rhizosphere of different potato cultivars: many common and few cultivar-dependent taxa. FEMS Microbiology Ecology, 2011, 75, 497-506.	2.7	198
201	Linking ecology with economy: Insights into polyhydroxyalkanoate-producing microorganisms. Engineering in Life Sciences, 2011, 11, 222-237.	3.6	101
202	Emerging multi-pathogen disease caused by <i>Didymella bryoniae</i> and pathogenic bacteria on Styrian oil pumpkin. European Journal of Plant Pathology, 2011, 131, 539-548.	1.7	22
203	Analysis of the endophytic lifestyle and plant growth promotion of <i>Burkholderia terricola</i> ZR2-12. Plant and Soil, 2011, 347, 125-136.	3.7	32
204	Bacteria able to control foot and root rot and to promote growth of cucumber in salinated soils. Biology and Fertility of Soils, 2011, 47, 197-205.	4.3	159
205	Structure and function of the symbiosis partners of the lung lichen ( <i>Lobaria pulmonaria</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 165	2.2	165
206	Functional and Structural Microbial Diversity in Organic and Conventional Viticulture: Organic Farming Benefits Natural Biocontrol Agents. Applied and Environmental Microbiology, 2011, 77, 2188-2191.	3.1	106
207	Similar Diversity of Alphaproteobacteria and Nitrogenase Gene Amplicons on Two Related Sphagnum Mosses. Frontiers in Microbiology, 2011, 2, 275.	3.5	60
208	Ecology and Human Pathogenicity of Plant-Associated Bacteria. , 2011, , 175-189.		12
209	Effects of genetically modified potatoes with increased zeaxanthin content on the abundance and diversity of rhizobacteria with in vitro antagonistic activity do not exceed natural variability among cultivars. Plant and Soil, 2010, 326, 437-452.	3.7	36
210	Strain-specific colonization pattern of <i>Rhizoctonia</i> antagonists in the root system of sugar beet. FEMS Microbiology Ecology, 2010, 74, 124-135.	2.7	78
211	Bacterial diversity on the surface of potato tubers in soil and the influence of the plant genotype. FEMS Microbiology Ecology, 2010, 74, 114-123.	2.7	46
212	Monitoring the plant epiphyte <i>Methylobacterium extorquens</i> DSM 21961 by real-time PCR and its influence on the strawberry flavor. FEMS Microbiology Ecology, 2010, 74, 136-145.	2.7	86
213	Development of a molecular approach to describe the composition of <i>Trichoderma</i> communities. Journal of Microbiological Methods, 2010, 80, 63-69.	1.6	32
214	Co-inoculation of <i>Pseudomonas</i> spp. with <i>Rhizobium</i> improves growth and symbiotic performance of fodder galega ( <i>Galega orientalis</i> Lam.). European Journal of Soil Biology, 2010, 46, 269-272.	3.2	103
215	Production of Volatile Metabolites by Grape-Associated Microorganisms. Journal of Agricultural and Food Chemistry, 2010, 58, 8344-8350.	5.2	119
216	Symbiotic Plant-Microbe Interactions: Stress Protection, Plant Growth Promotion, and Biocontrol by <i>Stenotrophomonas</i> . Cellular Origin and Life in Extreme Habitats, 2010, , 445-460.	0.3	42

#	ARTICLE	IF	CITATIONS
217	Rhizosphere Communities of Genetically Modified Zeaxanthin-Accumulating Potato Plants and Their Parent Cultivar Differ Less than Those of Different Potato Cultivars. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3859-3865.	3.1	122
218	Microbial consortia of bacteria and fungi with focus on the lichen symbiosis. <i>Fungal Biology Reviews</i> , 2009, 23, 72-85.	4.7	179
219	Plant-driven selection of microbes. <i>Plant and Soil</i> , 2009, 321, 235-257.	3.7	872
220	Induction of systemic resistance, root colonisation and biocontrol activities of the rhizospheric strain of <i>Serratia plymuthica</i> are dependent on N-acyl homoserine lactones. <i>European Journal of Plant Pathology</i> , 2009, 124, 261-268.	1.7	106
221	The <i>Caenorhabditis elegans</i> assay: a tool to evaluate the pathogenic potential of bacterial biocontrol agents. <i>European Journal of Plant Pathology</i> , 2009, 125, 367-376.	1.7	34
222	Plant-microbe interactions promoting plant growth and health: perspectives for controlled use of microorganisms in agriculture. <i>Applied Microbiology and Biotechnology</i> , 2009, 84, 11-18.	3.6	1,335
223	Species-specific structural and functional diversity of bacterial communities in lichen symbioses. <i>ISME Journal</i> , 2009, 3, 1105-1115.	9.8	303
224	The versatility and adaptation of bacteria from the genus <i>Stenotrophomonas</i> . <i>Nature Reviews Microbiology</i> , 2009, 7, 514-525.	28.6	641
225	Quorum-sensing effects in the antagonistic rhizosphere bacterium <i>Serratia plymuthica</i> HRO-C48. <i>FEMS Microbiology Ecology</i> , 2009, 67, 468-478.	2.7	126
226	Plant species and soil type cooperatively shape the structure and function of microbial communities in the rhizosphere. <i>FEMS Microbiology Ecology</i> , 2009, 68, 1-13.	2.7	1,879
227	Ecology and characterization of polyhydroxyalkanoate-producing microorganisms on and in plants. <i>FEMS Microbiology Ecology</i> , 2009, 70, 142-150.	2.7	39
228	Production of the antifungal compound pyrrolnitrin is quorum sensing-regulated in members of the <i>Burkholderia cepacia</i> complex. <i>Environmental Microbiology</i> , 2009, 11, 1422-1437.	3.8	106
229	Fungal diversity in the rhizosphere of endemic plant species of Tenerife (Canary Islands): relationship to vegetation zones and environmental factors. <i>ISME Journal</i> , 2009, 3, 79-92.	9.8	80
230	Characterization of plant growth promoting bacteria from crops in Bolivia. <i>Journal of Plant Diseases and Protection</i> , 2009, 116, 149-155.	2.9	31
231	Sugar Beet-Associated Bacterial and Fungal Communities Show a High Indigenous Antagonistic Potential Against Plant Pathogens. <i>Microbial Ecology</i> , 2008, 55, 119-129.	2.8	82
232	Impact of formulation procedures on the effect of the biocontrol agent <i>Serratia plymuthica</i> HRO-C48 on <i>Verticillium</i> wilt in oilseed rape. <i>BioControl</i> , 2008, 53, 905-916.	2.0	72
233	Effect of bacterial antagonists on lettuce: active biocontrol of <i>Rhizoctonia solani</i> and negligible, short-term effects on nontarget microorganisms. <i>FEMS Microbiology Ecology</i> , 2008, 64, 106-116.	2.7	98
234	In situ analysis of the bacterial community associated with the reindeer lichen <i>Cladonia arbuscula</i> reveals predominance of Alphaproteobacteria. <i>FEMS Microbiology Ecology</i> , 2008, 66, 63-71.	2.7	203

#	ARTICLE	IF	CITATIONS
235	The Plant-Associated Bacterium <i>Stenotrophomonas rhizophila</i> Expresses a New Enzyme for the Synthesis of the Compatible Solute Glucosylglycerol. <i>Journal of Bacteriology</i> , 2008, 190, 5898-5906.	2.2	47
236	<i>Burkholderia bryophila</i> sp. nov. and <i>Burkholderia megapolitana</i> sp. nov., moss-associated species with antifungal and plant-growth-promoting properties. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2228-2235.	1.7	87
237	Analysis of antagonistic interactions between <i>Trichoderma</i> isolates from Brazilian weeds and the soil-borne pathogen <i>Rhizoctonia solani</i> . <i>Journal of Plant Diseases and Protection</i> , 2007, 114, 167-175.	2.9	21
238	High specificity but contrasting biodiversity of <i>Sphagnum</i> -associated bacterial and plant communities in bog ecosystems independent of the geographical region. <i>ISME Journal</i> , 2007, 1, 502-516.	9.8	92
239	<i>Pseudomonas</i> community structure and antagonistic potential in the rhizosphere: insights gained by combining phylogenetic and functional gene-based analyses. <i>Environmental Microbiology</i> , 2007, 9, 2260-2273.	3.8	86
240	Investigations of the structure and function of bacterial communities associated with <i>Sphagnum</i> mosses. <i>Environmental Microbiology</i> , 2007, 9, 2795-2809.	3.8	116
241	The bryophyte genus <i>Sphagnum</i> is a reservoir for powerful and extraordinary antagonists and potentially facultative human pathogens. <i>FEMS Microbiology Ecology</i> , 2007, 61, 38-53.	2.7	70
242	Quorum-sensing signaling is required for production of the antibiotic pyrrolnitrin in a rhizospheric biocontrol strain of <i>Serratia plymuthica</i> . <i>FEMS Microbiology Letters</i> , 2007, 270, 299-305.	1.8	102
243	Volatiles of bacterial antagonists inhibit mycelial growth of the plant pathogen <i>Rhizoctonia solani</i> . <i>Archives of Microbiology</i> , 2007, 187, 351-360.	2.2	374
244	Assessing the Risk of Biological Control Agents on the Indigenous Microbial Communities: <i>Serratia plymuthica</i> HRO-C48 and <i>Streptomyces</i> sp. HRO-71 as Model Bacteria. <i>BioControl</i> , 2007, 52, 87-112.	2.0	36
245	Cultivation-independent analysis of <i>Pseudomonas</i> species in soil and in the rhizosphere of field-grown <i>Verticillium dahliae</i> host plants. <i>Environmental Microbiology</i> , 2006, 8, 2136-2149.	3.8	77
246	The rhizosphere effect on bacteria antagonistic towards the pathogenic fungus <i>Verticillium</i> differs depending on plant species and site. <i>FEMS Microbiology Ecology</i> , 2006, 56, 250-261.	2.7	158
247	Effects of site and plant species on rhizosphere community structure as revealed by molecular analysis of microbial guilds. <i>FEMS Microbiology Ecology</i> , 2006, 56, 236-249.	2.7	372
248	Survival of <i>gfp</i> -tagged antagonistic bacteria in the rhizosphere of tomato plants and their effects on the indigenous bacterial community. <i>FEMS Microbiology Ecology</i> , 2006, 56, 207-218.	2.7	83
249	Fungal endophytes in potato roots studied by traditional isolation and cultivation-independent DNA-based methods. <i>FEMS Microbiology Ecology</i> , 2006, 58, 404-413.	2.7	63
250	Impact of transgenic potatoes expressing anti-bacterial agents on bacterial endophytes is comparable with the effects of plant genotype, soil type and pathogen infection. <i>Journal of Applied Ecology</i> , 2006, 43, 555-566.	4.0	135
251	Spectrum and Population Dynamics of Bacterial Root Endophytes. , 2006, , 15-31.		90
252	Detection of a Phage Genome Carrying a <i>Zonula Occludens</i> like Toxin Gene ( <i>zot</i> ) in clinical isolates of <i>Stenotrophomonas maltophilia</i> . <i>Archives of Microbiology</i> , 2006, 185, 449-458.	2.2	48

#	ARTICLE	IF	CITATIONS
253	Diversity and antagonistic potential of <i>Pseudomonas</i> spp. associated to the rhizosphere of maize grown in a subtropical organic farm. <i>Soil Biology and Biochemistry</i> , 2006, 38, 2434-2447.	8.8	64
254	Fungal antagonists of the plant pathogen <i>Rhizoctonia solani</i> : selection, control efficacy and influence on the indigenous microbial community. <i>Mycological Research</i> , 2006, 110, 1464-1474.	2.5	75
255	Synthesis of the compatible solutes glucosylglycerol and trehalose by salt-stressed cells of <i>Stenotrophomonas</i> strains. <i>FEMS Microbiology Letters</i> , 2005, 243, 219-226.	1.8	66
256	The rhizosphere as a reservoir for opportunistic human pathogenic bacteria. <i>Environmental Microbiology</i> , 2005, 7, 1673-1685.	3.8	554
257	A molecular biological protocol to distinguish potentially human pathogenic <i>Stenotrophomonas maltophilia</i> from plant-associated <i>Stenotrophomonas rhizophila</i> . <i>Environmental Microbiology</i> , 2005, 7, 1853-1858.	3.8	36
258	Endophytic and ectophytic potato-associated bacterial communities differ in structure and antagonistic function against plant pathogenic fungi. <i>FEMS Microbiology Ecology</i> , 2005, 51, 215-229.	2.7	464
259	Impact of Plant Species and Site on Rhizosphere-Associated Fungi Antagonistic to <i>Verticillium dahliae</i> Kleb. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4203-4213.	3.1	185
260	Effectiveness of 3 antagonistic bacterial isolates to control <i>Rhizoctonia solani</i> K <sup>1</sup> /4hn on lettuce and potato. <i>Canadian Journal of Microbiology</i> , 2005, 51, 345-353.	1.7	97
261	Diversity and Antagonistic Potential of Bacteria Associated with Bryophytes from Nutrient-Poor Habitats of the Baltic Sea Coast. <i>Applied and Environmental Microbiology</i> , 2004, 70, 6569-6579.	3.1	123
262	Strategy to select and assess antagonistic bacteria for biological control of <i>Rhizoctonia solani</i> K <sup>1</sup> /4hn. <i>Canadian Journal of Microbiology</i> , 2004, 50, 811-820.	1.7	59
263	Endophytic bacterial communities of field-grown potato plants and their plant-growth-promoting and antagonistic abilities. <i>Canadian Journal of Microbiology</i> , 2004, 50, 239-249.	1.7	323
264	Mikrobielle Antagonisten in der Rhizosphäre: Diversität und Interaktionen. , 2003, , 55-60.		0
265	Identification and Characterization of an N -Acylhomoserine Lactone-Dependent Quorum-Sensing System in <i>Pseudomonas putida</i> Strain IsoF. <i>Applied and Environmental Microbiology</i> , 2002, 68, 6371-6382.	3.1	131
266	<i>Stenotrophomonas rhizophila</i> sp. nov., a novel plant-associated bacterium with antifungal properties.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 1937-1944.	1.7	145
267	Effects of T4 Lysozyme Release from Transgenic Potato Roots on Bacterial Rhizosphere Communities Are Negligible Relative to Natural Factors. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1325-1335.	3.1	192
268	Potato-associated bacteria and their antagonistic potential towards plant-pathogenic fungi and the plant-parasitic nematode <i>Meloidogyne incognita</i> (Kofoid & White) Chitwood. <i>Canadian Journal of Microbiology</i> , 2002, 48, 772-786.	1.7	165
269	Plant-Dependent Genotypic and Phenotypic Diversity of Antagonistic Rhizobacteria Isolated from Different <i>Verticillium</i> Host Plants. <i>Applied and Environmental Microbiology</i> , 2002, 68, 3328-3338.	3.1	345
270	Purification and properties of two chitinolytic enzymes of <i>Serratia plymuthica</i> HRO-C48. <i>Archives of Microbiology</i> , 2001, 176, 421-426.	2.2	211



#	ARTICLE	IF	CITATIONS
271	Phenotypic and genotypic characterization of antagonistic bacteria associated with roots of transgenic and non-transgenic potato plants. <i>Microbiological Research</i> , 2001, 156, 75-82.	5.3	55
272	Biological Control of Fungal Strawberry Diseases by <i>Serratia plymuthica</i> HRO-C48. <i>Plant Disease</i> , 2001, 85, 529-534.	1.4	101
273	Comparison of Antifungal Activities and 16S Ribosomal DNA Sequences of Clinical and Environmental Isolates of <i>Stenotrophomonas maltophilia</i> . <i>Journal of Clinical Microbiology</i> , 2001, 39, 139-145.	3.9	106
274	Establishment of introduced antagonistic bacteria in the rhizosphere of transgenic potatoes and their effect on the bacterial community. <i>FEMS Microbiology Ecology</i> , 2000, 33, 41-49.	2.7	121
275	Salt Adaptation in <i>Pseudomonads</i> : Characterization of Glucosylglycerol-Synthesizing Isolates from Brackish Coastal Waters and the Rhizosphere. <i>Systematic and Applied Microbiology</i> , 2000, 23, 31-40.	2.8	29
276	Successful strategy for the selection of new strawberry-associated rhizobacteria antagonistic to <i>Verticillium</i> wilt. <i>Canadian Journal of Microbiology</i> , 2000, 46, 1128-1137.	1.7	54
277	Influence of transgenic T4-lysozyme-producing potato plants on potentially beneficial plant-associated bacteria. <i>FEMS Microbiology Ecology</i> , 1999, 29, 365-377.	2.7	112
278	Ein Pink-Phänomen mykologischen Ursprungs. <i>Rechtsmedizin</i> , 1999, 10, 29-31.	0.8	1
279	Influence of transgenic T4-lysozyme-producing potato plants on potentially beneficial plant-associated bacteria. <i>FEMS Microbiology Ecology</i> , 1999, 29, 365-377.	2.7	6
280	Genotypic and Phenotypic Relationships between Clinical and Environmental Isolates of <i>Stenotrophomonas maltophilia</i> . <i>Journal of Clinical Microbiology</i> , 1999, 37, 3594-3600.	3.9	188
281	Population dynamics of bacteria including antifungal species in the rhizosphere of oilseed rape during its life cycle. <i>Archives of Phytopathology and Plant Protection</i> , 1998, 31, 215-224.	1.3	6
282	Maltophilin: A New Antifungal Compound Produced by <i>Stenotrophomonas maltophilia</i> R3089. <i>Journal of Antibiotics</i> , 1996, 49, 1101-1104.	2.0	137
283	Strains of the genus <i>Serratia</i> as beneficial rhizobacteria of oilseed rape with antifungal properties. <i>Microbiological Research</i> , 1996, 151, 433-439.	5.3	142
284	<i>Stenotrophomonas maltophilia</i> in the rhizosphere of oilseed rape – occurrence, characterization and interaction with phytopathogenic fungi. <i>Microbiological Research</i> , 1996, 151, 19-27.	5.3	113
285	Biological control of <i>Verticillium dahliae</i> Kleb. by natural occurring rhizosphere bacteria. <i>Archives of Phytopathology and Plant Protection</i> , 1994, 29, 249-262.	1.3	44
286	Bacterial Antagonists to <i>Verticillium dahliae</i> Kleb.. <i>Journal of Phytopathology</i> , 1994, 141, 99-110.	1.0	61
287	A Holistic Approach for Enhancing the Efficacy of Soil Microbial Inoculants in Agriculture. <i>Global Journal of Agricultural Innovation Research &amp; Development</i> , 0, 8, 176-190.	0.2	13
288	Microbiome Research as an Effective Driver of Success Stories in Agrifood Systems – A Selection of Case Studies. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	10