## Angela Sessitsch

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7246820/publications.pdf

Version: 2024-02-01

196 papers 25,513 citations

7096 78 h-index 153 g-index

205 all docs

205 docs citations

205 times ranked 19367 citing authors

#	Article	IF	Citations
1	The Hidden World within Plants: Ecological and Evolutionary Considerations for Defining Functioning of Microbial Endophytes. Microbiology and Molecular Biology Reviews, 2015, 79, 293-320.	6.6	1,895
2	Plant growth-promoting bacteria in the rhizo- and endosphere of plants: Their role, colonization, mechanisms involved and prospects for utilization. Soil Biology and Biochemistry, 2010, 42, 669-678.	8.8	1,806
3	Microbiome definition re-visited: old concepts and new challenges. Microbiome, 2020, 8, 103.	11.1	903
4	A review on the plant microbiome: Ecology, functions, and emerging trends in microbial application. Journal of Advanced Research, 2019, 19, 29-37.	9.5	850
5	Endophytic Colonization of Vitis vinifera L. by Plant Growth-Promoting Bacterium Burkholderia sp. Strain PsJN. Applied and Environmental Microbiology, 2005, 71, 1685-1693.	3.1	718
6	Microbial Population Structures in Soil Particle Size Fractions of a Long-Term Fertilizer Field Experiment. Applied and Environmental Microbiology, 2001, 67, 4215-4224.	3.1	623
7	Functional Characteristics of an Endophyte Community Colonizing Rice Roots as Revealed by Metagenomic Analysis. Molecular Plant-Microbe Interactions, 2012, 25, 28-36.	2.6	613
8	The role of plant-associated bacteria in the mobilization and phytoextraction of trace elements in contaminated soils. Soil Biology and Biochemistry, 2013, 60, 182-194.	8.8	566
9	Metabolic potential of endophytic bacteria. Current Opinion in Biotechnology, 2014, 27, 30-37.	6.6	496
10	Bacterial Communities Associated with Flowering Plants of the Ni Hyperaccumulator Thlaspi goesingense. Applied and Environmental Microbiology, 2004, 70, 2667-2677.	3.1	477
11	Climate change effects on beneficial plant-microorganism interactions. FEMS Microbiology Ecology, 2010, 73, no-no.	2.7	443
12	Endophytes of Grapevine Flowers, Berries, and Seeds: Identification of Cultivable Bacteria, Comparison with Other Plant Parts, and Visualization of Niches of Colonization. Microbial Ecology, 2011, 62, 188-197.	2.8	437
13	Increased drought stress resilience of maize through endophytic colonization by Burkholderia phytofirmans PsJN and Enterobacter sp. FD17. Environmental and Experimental Botany, 2014, 97, 30-39.	4.2	423
14	Ecology and Genomic Insights into Plant-Pathogenic and Plant-Nonpathogenic Endophytes. Annual Review of Phytopathology, 2017, 55, 61-83.	7.8	353
15	Belowground carbon allocation by trees drives seasonal patterns of extracellular enzyme activities by altering microbial community composition in a beech forest soil. New Phytologist, 2010, 187, 843-858.	7.3	337
16	Endophytic bacterial communities of field-grown potato plants and their plant-growth-promoting and antagonistic abilities. Canadian Journal of Microbiology, 2004, 50, 239-249.	1.7	323
17	Burkholderia phytofirmans sp. nov., a novel plant-associated bacterium with plant-beneficial properties. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 1187-1192.	1.7	322
18	A New Approach to Modify Plant Microbiomes and Traits by Introducing Beneficial Bacteria at Flowering into Progeny Seeds. Frontiers in Microbiology, 2017, 8, 11.	3.5	313

#	Article	IF	Citations
19	Endophytic bacteria: Prospects and applications for the phytoremediation of organic pollutants. Chemosphere, 2014, 117, 232-242.	8.2	308
20	Experimental warming effects on the microbial community of a temperate mountain forest soil. Soil Biology and Biochemistry, 2011, 43, 1417-1425.	8.8	294
21	Drought stress amelioration in wheat through inoculation with Burkholderia phytofirmans strain PsJN. Plant Growth Regulation, 2014, 73, 121-131.	3.4	286
22	Bacterial endophytes contribute to abiotic stress adaptation in pepper plants ( <i>Capsicum) Tj ETQq0 0 0 rgB1</i>	Overlock 1.7	10 <u>Tf</u> 50 622
23	Seasonality and resource availability control bacterial and archaeal communities in soils of a temperate beech forest. ISME Journal, 2011, 5, 389-402.	9.8	273
24	Development and validation of a diagnostic microbial microarray for methanotrophs. Environmental Microbiology, 2003, 5, 566-582.	3.8	269
25	Cultivation-independent population analysis of bacterial endophytes in three potato varieties based on eubacterial and Actinomycetes-specific PCR of 16S rRNA genes. FEMS Microbiology Ecology, 2002, 39, 23-32.	2.7	257
26	Response of Endophytic Bacterial Communities in Potato Plants to Infection with Erwinia carotovora subsp. atroseptica. Applied and Environmental Microbiology, 2002, 68, 2261-2268.	3.1	253
27	Rhizosphere bacteria affect growth and metal uptake of heavy metal accumulating willows. Plant and Soil, 2008, 304, 35-44.	3.7	247
28	Advances in Rhizobium Research. Critical Reviews in Plant Sciences, 2002, 21, 323-378.	5.7	246
29	Oligonucleotide microarrays in microbial diagnostics. Current Opinion in Microbiology, 2004, 7, 245-254.	5.1	241
30	Nitrifiers and denitrifiers respond rapidly to changed moisture and increasing temperature in a pristine forest soil. FEMS Microbiology Ecology, 2010, 72, 395-406.	2.7	228
31	Comparative genome analysis of Burkholderia phytofirmans PsJN reveals a wide spectrum of endophytic lifestyles based on interaction strategies with host plants. Frontiers in Plant Science, 2013, 4, 120.	3.6	219
32	Nitrogen fixation by phyllosphere bacteria associated with higher plants and their colonizing epiphytes of a tropical lowland rainforest of Costa Rica. ISME Journal, 2008, 2, 561-570.	9.8	218
33	Endophytic colonization of Vitis vinifera L. by Burkholderia phytofirmans strain PsJN: from the rhizosphere to inflorescence tissues. FEMS Microbiology Ecology, 2008, 63, 84-93.	2.7	213
34	Culturable bacteria from Zn- and Cd-accumulating <i>Salix caprea &lt; /i&gt; with differential effects on plant growth and heavy metal availability. Journal of Applied Microbiology, 2010, 108, 1471-1484.</i>	3.1	209
35	Optimization of diagnostic microarray for application in analysing landfill methanotroph communities under different plant covers. Environmental Microbiology, 2004, 6, 347-363.	3.8	183
36	Rice root-associated bacteria: insights into community structures across 10 cultivars. FEMS Microbiology Ecology, 2011, 77, 154-164.	2.7	183

#	Article	IF	Citations
37	Comparison of Diversities and Compositions of Bacterial Populations Inhabiting Natural Forest Soils. Applied and Environmental Microbiology, 2004, 70, 5057-5065.	3.1	179
38	Microbial processes and community composition in the rhizosphere of European beech–ÂThe influence of plant C exudates. Soil Biology and Biochemistry, 2011, 43, 551-558.	8.8	170
39	Soil type affects plant colonization, activity and catabolic gene expression of inoculated bacterial strains during phytoremediation of diesel. Journal of Hazardous Materials, 2011, 186, 1568-1575.	12.4	165
40	Hydrocarbon degradation, plant colonization and gene expression of alkane degradation genes by endophytic Enterobacter ludwigii strains. Environmental Pollution, 2011, 159, 2675-2683.	7.5	164
41	The Inoculation Method Affects Colonization and Performance of Bacterial Inoculant Strains in the Phytoremediation of Soil Contaminated with Diesel Oil. International Journal of Phytoremediation, 2012, 14, 35-47.	3.1	156
42	Microbiome Applications from Lab to Field: Facing Complexity. Trends in Plant Science, 2019, 24, 194-198.	8.8	153
43	The plant endosphere world – bacterial life within plants. Environmental Microbiology, 2021, 23, 1812-1829.	3.8	146
44	Complete Genome Sequence of the Plant Growth-Promoting Endophyte Burkholderia phytofirmans Strain PsJN. Journal of Bacteriology, 2011, 193, 3383-3384.	2.2	144
45	Rhizosphere bacteria affected by transgenic potatoes with antibacterial activities compared with the effects of soil, wild-type potatoes, vegetation stage and pathogen exposure. FEMS Microbiology Ecology, 2006, 56, 219-235.	2.7	143
46	Impact of transgenic potatoes expressing anti-bacterial agents on bacterial endophytes is comparable with the effects of plant genotype, soil type and pathogen infection. Journal of Applied Ecology, 2006, 43, 555-566.	4.0	135
47	The endophyte Enterobacter sp. FD17: a maize growth enhancer selected based on rigorous testing of plant beneficial traits and colonization characteristics. Biology and Fertility of Soils, 2014, 50, 249-262.	4.3	133
48	Transcriptome Profiling of the Endophyte Burkholderia phytofirmans PsJN Indicates Sensing of the Plant Environment and Drought Stress. MBio, 2015, 6, e00621-15.	4.1	132
49	Seasonal variation in functional properties of microbial communities in beech forest soil. Soil Biology and Biochemistry, 2013, 60, 95-104.	8.8	131
50	Maintenance and assessment of cell viability in formulation of nonâ€sporulating bacterial inoculants. Microbial Biotechnology, 2018, 11, 277-301.	4.2	131
51	Phylogenetic and functional diversity of alkane degrading bacteria associated with Italian ryegrass (Lolium multiflorum) and Birdsfoot trefoil (Lotus corniculatus) in a petroleum oil-contaminated environment. Journal of Hazardous Materials, 2010, 184, 523-532.	12.4	128
52	Effects of season and experimental warming on the bacterial community in a temperate mountain forest soil assessed by 16S rRNA gene pyrosequencing. FEMS Microbiology Ecology, 2012, 82, 551-562.	2.7	128
53	Genome mining: Prediction of lipopeptides and polyketides from Bacillus and related Firmicutes. Computational and Structural Biotechnology Journal, 2015, 13, 192-203.	4.1	127
54	Expression of alkane monooxygenase (alkB) genes by plant-associated bacteria in the rhizosphere and endosphere of Italian ryegrass (Lolium multiflorum L.) grown in diesel contaminated soil. Environmental Pollution, 2009, 157, 3347-3350.	<b>7.</b> 5	126

#	Article	IF	Citations
55	The Effect of Primer Choice and Short Read Sequences on the Outcome of 16S rRNA Gene Based Diversity Studies. PLoS ONE, 2013, 8, e71360.	2.5	121
56	Back to the Future of Soil Metagenomics. Frontiers in Microbiology, 2016, 7, 73.	3.5	120
57	Plants control the seasonal dynamics of microbial N cycling in a beech forest soil by belowground C allocation. Ecology, 2011, 92, 1036-1051.	3.2	118
58	Methylobacterium-Induced Endophyte Community Changes Correspond with Protection of Plants against Pathogen Attack. PLoS ONE, 2012, 7, e46802.	2.5	118
59	Cadmium-tolerant bacteria induce metal stress tolerance in cereals. Environmental Science and Pollution Research, 2014, 21, 11054-11065.	5.3	117
60	Micro-scale distribution of microorganisms and microbial enzyme activities in a soil with long-term organic amendment. European Journal of Soil Science, 2003, 54, 715-724.	3.9	115
61	Long-Range Surface Plasmon-Enhanced Fluorescence Spectroscopy Biosensor for Ultrasensitive Detection of <i>E. coli</i> ) O157:H7. Analytical Chemistry, 2011, 83, 674-677.	6.5	115
62	Cr-resistant rhizo- and endophytic bacteria associated with Prosopis juliflora and their potential as phytoremediation enhancing agents in metal-degraded soils. Frontiers in Plant Science, 2014, 5, 755.	3.6	114
63	Rhizosphere microbiomes of potato cultivated in the High Andes show stable and dynamic core microbiomes with different responses to plant development. FEMS Microbiology Ecology, 2017, 93, fiw242.	2.7	114
64	Use of beneficial bacteria and their secondary metabolites to control grapevine pathogen diseases. BioControl, 2013, 58, 435-455.	2.0	109
65	Fungal and bacterial utilization of organic substrates depends on substrate complexity and N availability. FEMS Microbiology Ecology, 2014, 87, 142-152.	2.7	108
66	21st century agriculture: integration of plant microbiomes for improved crop production and food security. Microbial Biotechnology, 2015, 8, 32-33.	4.2	101
67	Biocontrol activity of surfactin A purified from Bacillus NH-100 and NH-217 against rice bakanae disease. Microbiological Research, 2018, 209, 1-13.	5.3	101
68	Bacterial rhizosphere populations of black poplar and herbal plants to be used for phytoremediation of diesel fuel. Soil Biology and Biochemistry, 2002, 34, 1883-1892.	8.8	100
69	Shared and hostâ€specific microbiome diversity and functioning of grapevine and accompanying weed plants. Environmental Microbiology, 2017, 19, 1407-1424.	3.8	100
70	Surfactin variants mediate speciesâ€specific biofilm formation and root colonization in <i>Bacillus</i> Environmental Microbiology, 2016, 18, 2634-2645.	3.8	99
71	The urgent need for microbiology literacy in society. Environmental Microbiology, 2019, 21, 1513-1528.	3.8	99
72	Dynamics of ammonia-oxidizing communities in barley-planted bulk soil and rhizosphere following nitrate and ammonium fertilizer amendment. FEMS Microbiology Ecology, 2010, 74, 575-591.	2.7	93

#	Article	IF	CITATIONS
73	Effects of transgenic glufosinate-tolerant oilseed rape (Brassica napus) and the associated herbicide application on eubacterial and Pseudomonas communities in the rhizosphere. FEMS Microbiology Ecology, 2002, 41, 181-190.	2.7	91
74	Combined amendment of immobilizers and the plant growth-promoting strain Burkholderia phytofirmans PsJN favours plant growth and reduces heavy metal uptake. Soil Biology and Biochemistry, 2015, 91, 140-150.	8.8	88
75	EndophyticnifHgene diversity in African sweet potato. Canadian Journal of Microbiology, 2003, 49, 549-555.	1.7	87
76	mRNA-Based Parallel Detection of Active Methanotroph Populations by Use of a Diagnostic Microarray. Applied and Environmental Microbiology, 2006, 72, 1672-1676.	3.1	87
77	Advances in Elucidating Beneficial Interactions Between Plants, Soil, and Bacteria. Advances in Agronomy, 2013, , 381-445.	5.2	86
78	The genomes of closely related Pantoea ananatis maize seed endophytes having different effects on the host plant differ in secretion system genes and mobile genetic elements. Frontiers in Microbiology, 2015, 6, 440.	3.5	85
79	RNA isolation from soil for bacterial community and functional analysis: evaluation of different extraction and soil conservation protocols. Journal of Microbiological Methods, 2002, 51, 171-179.	1.6	84
80	Diagnostic microbial microarrays in soil ecology. New Phytologist, 2006, 171, 719-736.	7.3	83
81	Hydrocarbon degradation and plant colonization by selected bacterial strains isolated from Italian ryegrass and birdsfoot trefoil. Journal of Applied Microbiology, 2010, 109, 1389-1401.	3.1	82
82	Characterization of Ni-tolerant methylobacteria associated with the hyperaccumulating plant Thlaspi goesingense and description of Methylobacterium goesingense sp. nov Systematic and Applied Microbiology, 2006, 29, 634-644.	2.8	81
83	Bacterial endophytes of the wildflowerCrocus albiflorusanalyzed by characterization of isolates and by a cultivation-independent approach. Canadian Journal of Microbiology, 2006, 52, 140-149.	1.7	77
84	The role of plant–microbiome interactions in weed establishment and control. FEMS Microbiology Ecology, 2016, 92, fiw138.	2.7	77
85	Chilling and cultivar type affect the diversity of bacterial endophytes colonizing sweet pepper (Capsicum anuumL.). Canadian Journal of Microbiology, 2006, 52, 1036-1045.	1.7	76
86	Evaluation of quantitative PCR combined with PMA treatment for molecular assessment of microbial water quality. Water Research, 2014, 67, 367-376.	11.3	73
87	Plant–microbe partnerships in 2020. Microbial Biotechnology, 2016, 9, 635-640.	4.2	72
88	Qualitative analysis of biosurfactants from Bacillus species exhibiting antifungal activity. PLoS ONE, 2018, 13, e0198107.	2.5	71
89	Heritability and Functional Importance of the <i>Setaria viridis</i> Bacterial Seed Microbiome. Phytobiomes Journal, 2020, 4, 40-52.	2.7	71
90	Beneficial Endophytic Bacteria-Serendipita indica Interaction for Crop Enhancement and Resistance to Phytopathogens. Frontiers in Microbiology, 2019, 10, 2888.	3.5	70

#	Article	IF	CITATIONS
91	Community profiling and gene expression of fungal assimilatory nitrate reductases in agricultural soil. ISME Journal, 2011, 5, 1771-1783.	9.8	67
92	Interactions between accumulation of trace elements and macronutrients in Salix caprea after inoculation with rhizosphere microorganisms. Chemosphere, 2011, 84, 1256-1261.	8.2	66
93	Commentary: seed bacterial inhabitants and their routes of colonization. Plant and Soil, 2018, 422, 129-134.	3.7	66
94	L-Tryptophan-dependent biosynthesis of indole-3-acetic acid (IAA) improves plant growth and colonization of maize by Burkholderia phytofirmans PsJN. Annals of Microbiology, 2015, 65, 1381-1389.	2.6	65
95	Effects of level and quality of organic matter input on carbon storage and biological activity in soil: Synthesis of a long-term experiment. Global Biogeochemical Cycles, 2004, 18, n/a-n/a.	4.9	61
96	A microbial diagnostic microarray technique for the sensitive detection and identification of pathogenic bacteria in a background of nonpathogens. Analytical Biochemistry, 2007, 360, 244-254.	2.4	60
97	Rapid and dissimilar response of ammonia oxidizing archaea and bacteria to nitrogen and water amendment in two temperate forest soils. Microbiological Research, 2012, 167, 103-109.	5.3	60
98	Characterization of endophytic bacteria from cucurbit fruits with potential benefits to agriculture in melons ( <i>Cucumis melo</i> L.). FEMS Microbiology Ecology, 2015, 91, fiv074.	2.7	60
99	Plants Assemble Species Specific Bacterial Communities from Common Core Taxa in Three Arcto-Alpine Climate Zones. Frontiers in Microbiology, 2017, 8, 12.	3.5	60
100	Improved groupâ€specific primers based on the full <scp>SILVA</scp> 16 <scp>S</scp> r <scp>RNA</scp> gene reference database. Environmental Microbiology, 2014, 16, 2389-2407.	3.8	59
101	Next generation microbiome applications for crop production â€" limitations and the need of knowledge-based solutions. Current Opinion in Microbiology, 2019, 49, 59-65.	5.1	59
102	Molecular ecology of microbes: A review of promises, pitfalls and true progress. FEMS Microbiology Reviews, 1994, 15, 185-194.	8.6	58
103	Bacterial niches inside seeds of Cucumis melo L Plant and Soil, 2018, 422, 101-113.	3.7	58
104	Metagenomic analysis of the 1-aminocyclopropane-1-carboxylate deaminase gene (acdS) operon of an uncultured bacterial endophyte colonizing Solanum tuberosum L. Archives of Microbiology, 2011, 193, 665-676.	2.2	56
105	Genetically modified Bt maize lines containing cry3Bb1, cry1A105 or cry1Ab2 do not affect the structure and functioning of root-associated endophyte communities. Applied Soil Ecology, 2012, 54, 39-48.	4.3	56
106	Ochrobactrum rhizosphaerae sp. nov. and Ochrobactrum thiophenivorans sp. nov., isolated from the environment. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1426-1431.	1.7	55
107	The new species Enterobacter oryziphilus sp. nov. and Enterobacter oryzendophyticus sp. nov. are key inhabitants of the endosphere of rice. BMC Microbiology, 2013, 13, 164.	3.3	55
108	Biocontrol and plant growth promoting properties of Streptomyces mutabilis strain IA1 isolated from a Saharan soil on wheat seedlings and visualization of its niches of colonization. South African Journal of Botany, 2016, 105, 234-239.	2.5	55

#	Article	IF	Citations
109	Structural characteristics and plant-beneficial effects of bacteria colonizing the shoots of field grown conventional and genetically modified T4-lysozyme producing potatoes. Plant and Soil, 2006, 289, 123-140.	3.7	54
110	Interkingdom Transfer of the Acne-Causing Agent, Propionibacterium acnes, from Human to Grapevine. Molecular Biology and Evolution, 2014, 31, 1059-1065.	8.9	54
111	DNAâ€based stable isotope probing enables the identification of active bacterial endophytes in potatoes. New Phytologist, 2009, 181, 802-807.	7.3	53
112	Microbiome innovations for a sustainable future. Nature Microbiology, 2021, 6, 138-142.	13.3	53
113	MLST-v, multilocus sequence typing based on virulence genes, for molecular typing of Salmonella enterica subsp. enterica serovars. Journal of Microbiological Methods, 2007, 69, 23-36.	1.6	49
114	Activity of microorganisms in the rhizosphere of herbicide treated and untreated transgenic glufosinate-tolerant and wildtype oilseed rape grown in containment. Plant and Soil, 2005, 266, 105-116.	3.7	46
115	Grapevine colonization by endophytic bacteria shifts secondary metabolism and suggests activation of defense pathways. Plant and Soil, 2016, 405, 155-175.	3.7	46
116	The 125th anniversary of the first postulation of the soil origin of endophytic bacteria – a tribute to M.L.V. Galippe. Plant and Soil, 2012, 356, 299-301.	3.7	45
117	Diversity and community structure of culturable Bacillus spp. populations in the rhizospheres of transgenic potatoes expressing the lytic peptide cecropin B. Applied Soil Ecology, 2003, 22, 149-158.	4.3	44
118	16S rRNA based T-RFLP analysis of methane oxidising bacteriaâ€"Assessment, critical evaluation of methodology performance and application for landfill site cover soils. Applied Soil Ecology, 2006, 31, 251-266.	4.3	44
119	Bacterially Induced Weathering of Ultramafic Rock and Its Implications for Phytoextraction. Applied and Environmental Microbiology, 2013, 79, 5094-5103.	3.1	44
120	Spirosoma endophyticum sp. nov., isolated from Zn- and Cd-accumulating Salix caprea. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 4586-4590.	1.7	44
121	The Role of Microbial Inoculants in Integrated Crop Management Systems. Potato Research, 2014, 57, 291-309.	2.7	42
122	Contrasting response of two forest soils to nitrogen input: rapidly altered NO and N2O emissions and nirK abundance. Biology and Fertility of Soils, 2009, 45, 855-863.	4.3	41
123	The potential of plant microbiota in reducing postharvest food loss. Microbial Biotechnology, 2018, 11, 971-975.	4.2	39
124	The bacterial community in potato is recruited from soil and partly inherited across generations. PLoS ONE, 2019, 14, e0223691.	2.5	39
125	Characterization of Rhizobium etli and other Rhizobium spp. that nodulate Phaseolus vulgaris L. in an Austrian soil. Molecular Ecology, 1997, 6, 601-608.	3.9	38
126	Endophytic Pseudomonas spp. populations of pathogen-infected potato plants analysed by 16S rDNA-and 16S rRNA-based denaturating gradient gel electrophoresis. Plant and Soil, 2003, 257, 397-405.	3.7	38

#	Article	IF	CITATIONS
127	Grazing affects methanotroph activity and diversity in an alpine meadow soil. Environmental Microbiology Reports, 2009, 1, 457-465.	2.4	38
128	Greenhouse gas fluxes respond to different N fertilizer types due to altered plant-soil-microbe interactions. Plant and Soil, 2011, 343, 17-35.	3.7	37
129	Persistence and spread of Salmonella enterica serovar Weltevreden in soil and on spinach plants. FEMS Microbiology Letters, 2011, 314, 67-74.	1.8	36
130	Diversity of abundant bacteria in subsurface vertical flow constructed wetlands. Ecological Engineering, 2009, 35, 1021-1025.	3.6	35
131	Analysis of methanotroph community composition using a pmoA-based microbial diagnostic microarray. Nature Protocols, 2011, 6, 609-624.	12.0	34
132	The contribution of plant microbiota to economy growth. Microbial Biotechnology, 2018, 11, 801-805.	4.2	34
133	Measurement of the competitiveness index of Rhizobium tropici strain CIAT899 derivatives marked with the gusA gene. Soil Biology and Biochemistry, 1997, 29, 1099-1110.	8.8	33
134	Antimicrobial drimane sesquiterpenes and their effect on endophyte communities in the medical tree Warburgia ugandensis. Frontiers in Microbiology, 2014, 5, 13.	3.5	33
135	Regulon Studies and <i>In Planta</i> Role of the Bral/R Quorum-Sensing System in the Plant-Beneficial Burkholderia Cluster. Applied and Environmental Microbiology, 2013, 79, 4421-4432.	3.1	32
136	Major changes in grapevine wood microbiota are associated with the onset of esca, a devastating trunk disease. Environmental Microbiology, 2020, 22, 5189-5206.	3.8	32
137	Comparative Genomics of Microbacterium Species to Reveal Diversity, Potential for Secondary Metabolites and Heavy Metal Resistance. Frontiers in Microbiology, 2020, 11, 1869.	3.5	29
138	Use of marker genes in competition studies of Rhizobium. Plant and Soil, 1998, 204, 35-45.	3.7	28
139	The Rhizosphere: â€Â~soil compartment influenced by the root'. FEMS Microbiology Ecology, 2006, 56 165-165.	' 2.7	28
140	Effect of different heterotrophic plate count methods on the estimation of the composition of the culturable microbial community. PeerJ, 2015, 3, e862.	2.0	27
141	Interaction between endophytic Proteobacteria strains and Serendipita indica enhances biocontrol activity against fungal pathogens. Plant and Soil, 2020, 451, 277-305.	3.7	27
142	Deciphering the Niches of Colonisation of Vitis vinifera L. by the Esca-Associated Fungus Phaeoacremonium aleophilum Using a gfp Marked Strain and Cutting Systems. PLoS ONE, 2015, 10, e0126851.	2.5	27
143	A cost-effective high-throughput microcosm system for studying nitrogen dynamics at the plant-microbe-soil interface. Plant and Soil, 2009, 317, 293-307.	3.7	26
144	Microbial Diagnostic Microarrays for the Detection and Typing of Food- and Water-Borne (Bacterial) Pathogens. Microarrays (Basel, Switzerland), 2012, 1, 3-24.	1.4	25

#	Article	IF	Citations
145	Simultaneous detection of different Rhizobium strains marked with either the Escherichia coli gusA gene or the Pyrococcus furiosus celB gene. Applied and Environmental Microbiology, 1996, 62, 4191-4194.	3.1	25
146	Title is missing!. Plant and Soil, 1998, 204, 147-154.	3.7	24
147	Comparative genome analysis of the vineyard weed endophyte Pseudomonas viridiflava CDRTc14 showing selective herbicidal activity. Scientific Reports, 2017, 7, 17336.	3.3	24
148	Secondary metabolite genes encoded by potato rhizosphere microbiomes in the Andean highlands are diverse and vary with sampling site and vegetation stage. Scientific Reports, 2017, 7, 2330.	3.3	23
149	Bacterial Community Changes and Enrichment of Burkholderia-like Bacteria Induced by Chlorinated Benzoates in a Peat-Forest Soil-Microcosm. Systematic and Applied Microbiology, 2000, 23, 591-598.	2.8	22
150	Microbial ecology of biogeochemical interfaces - diversity, structure, and function of microhabitats in soil. FEMS Microbiology Ecology, 2013, 86, 1-2.	2.7	22
151	Endophytes and Rhizosphere Bacteria of Plants Growing in Heavy Metal-Containing Soils. Soil Biology, 2008, , 317-332.	0.8	21
152	Draft Genome Sequence of Biocontrol Agent <i>Pythium oligandrum</i> Strain Po37, an Oomycota. Genome Announcements, 2016, 4, .	0.8	21
153	Agromyces aureus sp. nov., isolated from the rhizosphere of Salix caprea L. grown in a heavy-metal-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3749-3754.	1.7	21
154	Remarkable Recovery and Colonization Behaviour of Methane Oxidizing Bacteria in Soil After Disturbance Is Controlled by Methane Source Only. Microbial Ecology, 2014, 68, 259-270.	2.8	20
155	Humic Acid Enhances the Growth of Tomato Promoted by Endophytic Bacterial Strains Through the Activation of Hormone-, Growth-, and Transcription-Related Processes. Frontiers in Plant Science, 2020, 11, 582267.	3.6	20
156	Analysis of Phaseolus–Rhizobium interactions in a subsistence farming system. Plant and Soil, 1998, 204, 107-115.	3.7	19
157	High-sensitivity, polymerase chain reaction-free detection of microorganisms and their functional genes using 70-mer oligonucleotide diagnostic microarray. Analytical Biochemistry, 2005, 346, 333-335.	2.4	19
158	Microbial diagnostic microarray for food―and waterâ€borne pathogens. Microbial Biotechnology, 2010, 3, 444-454.	4.2	19
159	Draft Genome Sequences of 10 <i>Microbacterium</i> spp., with Emphasis on Heavy Metal-Contaminated Environments. Genome Announcements, 2015, 3, .	0.8	19
160	Plants control the seasonal dynamics of microbial N cycling in a beech forest soil by belowground C allocation. Ecology, 2011, 92, 1036-1051.	3.2	19
161	Characterization of Two Bacterial Hydroxynitrile Lyases with High Similarity to Cupin Superfamily Proteins. Applied and Environmental Microbiology, 2012, 78, 2053-2055.	3.1	18
162	Calling for a systems approach in microbiome research and innovation. Current Opinion in Biotechnology, 2022, 73, 171-178.	6.6	18

#	Article	IF	Citations
163	Draft Genome Sequence of <i>Phaeomoniella chlamydospora</i> Strain RR-HG1, a Grapevine Trunk Disease (Esca)-Related Member of the Ascomycota. Genome Announcements, 2014, 2, .	0.8	17
164	Development of an oligonucleotide microarray method for <i>Salmonella</i> serotyping. Microbial Biotechnology, 2008, 1, 513-522.	4.2	16
165	SPR bacterial pathogen biosensor: The importance of fluidic conditions and probing depth. Talanta, 2014, 122, 166-171.	5.5	16
166	16S rRNA gene-based microbiome analysis identifies candidate bacterial strains that increase the storage time of potato tubers. Scientific Reports, 2021, 11, 3146.	3.3	16
167	Complete genome sequence of the heavy metal resistant bacterium Agromyces aureus AR33T and comparison with related Actinobacteria. Standards in Genomic Sciences, 2017, 12, 2.	1.5	15
168	Roots and Panicles of the C4 Model Grasses Setaria viridis (L). and S. pumila Host Distinct Bacterial Assemblages With Core Taxa Conserved Across Host Genotypes and Sampling Sites. Frontiers in Microbiology, 2018, 9, 2708.	3.5	15
169	Propidium monoazide–quantitative polymerase chain reaction for viable Escherichia coli and Pseudomonas detection from abundant background microflora. Analytical Biochemistry, 2013, 441, 69-72.	2.4	14
170	Response of organic matter pools and enzyme activities in particle size fractions to organic amendments in a long-term field experiment. Developments in Soil Science, 2002, , 329-344.	0.5	12
171	Combining microdilution with MicroRespâ,,¢: Microbial substrate utilization, antimicrobial susceptibility and respiration. Journal of Microbiological Methods, 2012, 88, 399-412.	1.6	12
172	High-Quality Draft Genome Sequence of an Endophytic Pseudomonas viridiflava Strain with Herbicidal Properties against Its Host, the Weed <i>Lepidium draba</i>	0.8	12
173	miCROPe 2019 $\hat{a}$ emerging research priorities towards microbe-assisted crop production. FEMS Microbiology Ecology, 2020, 96, .	2.7	12
174	Use of marker genes in competition studies of Rhizobium., 1998,, 35-45.		12
175	Microarray Analysis Reveals the Actual Specificity of Enrichment Media Used for Food Safety Assessment. Journal of Food Protection, 2011, 74, 1030-1034.	1.7	11
176	Potential of Rhizosphere Bacteria for Improving Rhizobium-Legume Symbiosis., 2013,, 305-349.		11
177	In-depth genome analysis of Bacillus sp. BH32, a salt stress-tolerant endophyte obtained from a halophyte in a semiarid region. Applied Microbiology and Biotechnology, 2022, 106, 3113-3137.	3.6	11
178	Beneficial Insects Deliver Plant Growth-Promoting Bacterial Endophytes between Tomato Plants. Microorganisms, 2021, 9, 1294.	3.6	10
179	Microbiome Research as an Effective Driver of Success Stories in Agrifood Systems $\hat{a}\in$ A Selection of Case Studies. Frontiers in Microbiology, 0, 13, .	3.5	10
180	Synergistic effects of microbial anaerobic dechlorination of perchloroethene and nano zero-valent iron (nZVI) – A lysimeter experiment. New Biotechnology, 2020, 57, 34-44.	4.4	9

#	Article	IF	Citations
181	Molecular diversity in the bacterial community and the fluorescent pseudomonads group in natural and chlorobenzoate-stressed peat-forest soil. Microbiological Research, 2003, 158, 47-54.	5.3	8
182	Persistence of Two <i>Campylobacter jejuni</i> Strains in Soil and on Spinach Plants. Applied and Environmental Soil Science, 2011, 2011, 1-7.	1.7	7
183	Towards a unified data infrastructure to support European and global microbiome research: a call to action. Environmental Microbiology, 2021, 23, 372-375.	3.8	7
184	Effects of transgenic glufosinate-tolerant oilseed rape (Brassica napus) and the associated herbicide application on eubacterial and Pseudomonas communities in the rhizosphere. FEMS Microbiology Ecology, 2002, 41, 181-190.	2.7	7
185	Variations in fungal community structure along elevation gradients in contrasting Austrian Alpine ecosystems. Applied Soil Ecology, 2022, 177, 104508.	4.3	7
186	Cultivation-independent population analysis of bacterial endophytes in three potato varieties based on eubacterial and Actinomycetes-specific PCR of 16S rRNA genes. FEMS Microbiology Ecology, 2002, 39, 23-32.	2.7	6
187	Verocytotoxin-producing Escherichia coli in Chamois (Rupicapra rupicapra) and Cattle in Austria. Journal of Wildlife Diseases, 2011, 47, 704-708.	0.8	3
188	Editorial: Special thematic issue on microbe-assisted crop production. FEMS Microbiology Ecology, 2016, 92, fiw167.	2.7	3
189	The Draft Genome Sequence of Paenibacillus polymyxa Strain CCI-25 Encompasses High Potential for Secondary Metabolite Production. Genome Announcements, 2016, 4, .	0.8	3
190	Editorial to the Thematic Topic "Towards a more sustainable agriculture through managing soil microbiomes― FEMS Microbiology Ecology, 2021, 97, .	2.7	3
191	Meeting Report: 1st International Functional Metagenomics Workshop May 7–8, 2012, St. Jacobs, Ontario, Canada Standards in Genomic Sciences, 2013, 8, 106-111.	1.5	2
192	Environmental Impact of Genetically Modified Maize Expressing Cry1 Proteins. Biotechnology in Agriculture and Forestry, 2010, , 575-614.	0.2	2
193	Phage-type specific markers identified by Diversity Arrays Technology (DArT) analysis of Salmonella enterica ssp. enterica serovars Enteritidis and Typhimurium. Journal of Microbiological Methods, 2010, 80, 100-105.	1.6	1
194	Antimicrobial Drimane Sesquiterpenes Contribute to Balanced Antagonism but Do Not Structure Bacterial and Fungal Endophytes in the African Pepper Bark Tree Warburgia ugandensis. Frontiers in Ecology and Evolution, 2017, 5, .	2.2	1
195	Oligonucleotide microarrays in microbial diagnostics. Current Opinion in Microbiology, 2004, 7, 245-245.	5.1	0
196	Literature search and data collection on RA for human health for microorganisms used as plant protection products. EFSA Supporting Publications, 2015, 12, 801E.	0.7	0