Kiwamu Minamisawa

List of Publications by Year
in descending order

185 papers	8,818 citations	38720 50 h-index	56687 83 g-index
186 all docs	186 docs citations	186 times ranked	6832 citing authors

#	Article	IF	Citations
1	Evolution of rhizobial symbiosis islands through insertion sequence-mediated deletion and duplication. ISME Journal, 2022, 16, 112-121.	4.4	12
2	<i>In Vivo</i> Evidence of Single ¹³ C and ¹⁵ N Isotopeâ€"Labeled Methanotrophic Nitrogen-Fixing Bacterial Cells in Rice Roots. MBio, 2022, 13, .	1.8	4
3	Community Analysis-based Screening of Plant Growth-promoting Bacteria for Sugar Beet. Microbes and Environments, 2021, 36, n/a.	0.7	18
4	Diversity of <i>Bradyrhizobium</i> in Non-Leguminous Sorghum Plants: <i>B. ottawaense</i> Isolates Unique in Genes for N₂O Reductase and Lack of the Type VI Secretion System. Microbes and Environments, 2020, 35, n/a.	0.7	16
5	Strains of Bradyrhizobium cosmicum sp. nov., isolated from contrasting habitats in Japan and Canada possess photosynthesis gene clusters with the hallmark of genomic islands. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5063-5074.	0.8	15
6	Levels of Periplasmic Nitrate Reductase during Denitrification are Lower in <i>Bradyrhizobium japonicum</i> than in <i>Bradyrhizobium diazoefficiens</i>. Microbes and Environments, 2020, 35, n/a.	0.7	1
7	Growth Stage-dependent Bacterial Communities in Soybean Plant Tissues: <i>Methylorubrum</i> Transiently Dominated in the Flowering Stage of the Soybean Shoot. Microbes and Environments, 2019, 34, 446-450.	0.7	19
8	Identification of Genes Regulated by the Antitermination Factor NasT during Denitrification in <i>Bradyrhizobium diazoefficiens</i>. Microbes and Environments, 2019, 34, 260-267.	0.7	2
9	Editorial: Metabolic Adjustments and Gene Expression Reprogramming for Symbiotic Nitrogen Fixation in Legume Nodules. Frontiers in Plant Science, 2019, 10, 898.	1.7	6
10	Molecular Analyses of the Distribution and Function of Diazotrophic Rhizobia and Methanotrophs in the Tissues and Rhizosphere of Non-Leguminous Plants. Plants, 2019, 8, 408.	1.6	21
11	Nitrogen Cycling in Soybean Rhizosphere: Sources and Sinks of Nitrous Oxide (N2O). Frontiers in Microbiology, 2019, 10, 1943.	1.5	28
12	Symbiotic incompatibility between soybean and Bradyrhizobium arises from one amino acid determinant in soybean Rj2 protein. PLoS ONE, 2019, 14, e0222469.	1.1	10
13	CH4 oxidation-dependent 15N2 fixation in rice roots in a low-nitrogen paddy field and in Methylosinus sp. strain 3S-1 isolated from the roots. Soil Biology and Biochemistry, 2019, 132, 40-46.	4.2	21
14	Identification of Nitrogen-Fixing Bradyrhizobium Associated With Roots of Field-Grown Sorghum by Metagenome and Proteome Analyses. Frontiers in Microbiology, 2019, 10, 407.	1.5	64
15	How will plant science contribute to improve productivity in agriculture?â€"Future prospects of plant scienceâ€". Ikushugaku Kenkyu, 2019, 21, 49-54.	0.1	0
16	Plant-Associated Microbes: From Rhizobia To Plant Microbiomes. Microbes and Environments, 2018, 33, 1-3.	0.7	24
17	Redundant roles of Bradyrhizobium oligotrophicum Cu-type (NirK) and cd1-type (NirS) nitrite reductase genes under denitrifying conditions. FEMS Microbiology Letters, 2018, 365, .	0.7	44
18	Core microbiomes for sustainable agroecosystems. Nature Plants, 2018, 4, 247-257.	4.7	639

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19	Mapping of quantitative trait loci related to primary rice root growth as a response to inoculation with Azospirillum sp. strain B510. Communicative and Integrative Biology, 2018, 11, 1-6.	0.6	3
20	Involvement of ethylene signaling in Azospirillum sp. B510-induced disease resistance in rice. Bioscience, Biotechnology and Biochemistry, 2018, 82, 1522-1526.	0.6	31
21	Variation in bradyrhizobial NopP effector determines symbiotic incompatibility with Rj2-soybeans via effector-triggered immunity. Nature Communications, 2018, 9, 3139.	5.8	88
22	Regulation of nitrous oxide reductase genes by NasTâ€mediated transcription antitermination in <i>Bradyrhizobium diazoefficiens</i>. Environmental Microbiology Reports, 2017, 9, 389-396.	1.0	10
23	Complete Genome Sequence of <i>Bradyrhizobium diazoefficiens</i> USDA 122, a Nitrogen-Fixing Soybean Symbiont. Genome Announcements, 2017, 5, .	0.8	9
24	Effects of colonization of a bacterial endophyte, <i>Azospirillum</i> sp. B510, on disease resistance in tomato. Bioscience, Biotechnology and Biochemistry, 2017, 81, 1657-1662.	0.6	18
25	Exploration of bacterial N₂-fixation systems in association with soil-grown sugarcane, sweet potato, and paddy rice: a review and synthesis. Soil Science and Plant Nutrition, 2017, 63, 578-590.	0.8	58
26	Assessment of bacterial communities of black soybean grown in fields. Communicative and Integrative Biology, 2017, 10, e1378290.	0.6	5
27	Complete Genome Sequence of Bradyrhizobium japonicum J5, Isolated from a Soybean Nodule in Hokkaido, Japan. Genome Announcements, 2017, 5, .	0.8	2
28	Effect of Flooding and the <i>nosZ</i> Gene in Bradyrhizobia on Bradyrhizobial Community Structure in the Soil. Microbes and Environments, 2017, 32, 154-163.	0.7	20
29	Anaerobic Reduction of Nitrate to Nitrous Oxide Is Lower in <i>Bradyrhizobium japonicum</i> than in <i>Bradyrhizobium diazoefficiens</i>. Microbes and Environments, 2017, 32, 398-401.	0.7	20
30	Expression of Two RpoH Sigma Factors in <i>Sinorhizobium meliloti</i> upon Heat Shock. Microbes and Environments, 2017, 32, 394-397.	0.7	3
31	Nitrate Supply-Dependent Shifts in Communities of Root-Associated Bacteria in <i>Arabidopsis</i>. Microbes and Environments, 2017, 32, 314-323.	0.7	9
32	Complete Genome Sequence of Methylobacterium sp. Strain AMS5, an Isolate from a Soybean Stem. Genome Announcements, 2016, 4, .	0.8	7
33	Origin and Evolution of Nitrogen Fixation Genes on Symbiosis Islands and Plasmid in <i>Bradyrhizobium</i>. Microbes and Environments, 2016, 31, 260-267.	0.7	42
34	Nitrogen fixation and nifH diversity in human gut microbiota. Scientific Reports, 2016, 6, 31942.	1.6	40
35	Draft Genome Sequence of <i>Methylosinus</i> sp. Strain 3S-1, an Isolate from Rice Root in a Low-Nitrogen Paddy Field. Genome Announcements, 2016, 4, .	0.8	8
36	Metagenomic Analysis Revealed Methylamine and Ureide Utilization of Soybean-Associated <i>Methylobacterium</i>. Microbes and Environments, 2016, 31, 268-278.	0.7	21

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37	Sulfur Fertilization Changes the Community Structure of Rice Root-, and Soil- Associated Bacteria. Microbes and Environments, 2016, 31, 70-75.	0.7	20
38	Identification of the Hydrogen Uptake Gene Cluster for Chemolithoautotrophic Growth and Symbiosis Hydrogen Uptake in <i>Bradyrhizobium Diazoefficiens</i>. Microbes and Environments, 2016, 31, 76-78.	0.7	9
39	Are Symbiotic Methanotrophs Key Microbes for N Acquisition in Paddy Rice Root?. Microbes and Environments, 2016, 31, 4-10.	0.7	36
40	Growth Rate of and Gene Expression in <i>Bradyrhizobium diazoefficiens</i> USDA110 due to a Mutation in blr7984, a TetR Family Transcriptional Regulator Gene. Microbes and Environments, 2016, 31, 249-259.	0.7	5
41	Mitigation of soil N2O emission by inoculation with a mixed culture of indigenous Bradyrhizobium diazoefficiens. Scientific Reports, 2016, 6, 32869.	1.6	57
42	A Sinorhizobium meliloti RpoH-Regulated Gene Is Involved in Iron-Sulfur Protein Metabolism and Effective Plant Symbiosis under Intrinsic Iron Limitation. Journal of Bacteriology, 2016, 198, 2297-2306.	1.0	19
43	Visualization of NO3âˆ’/NO2âˆ’ Dynamics in Living Cells by Fluorescence Resonance Energy Transfer (FRET) Imaging Employing a Rhizobial Two-component Regulatory System. Journal of Biological Chemistry, 2016, 291, 2260-2269.	1.6	17
44	Metagenomic Analysis of the Bacterial Community Associated with the Taproot of Sugar Beet. Microbes and Environments, 2015, 30, 63-69.	0.7	63
45	Possible Role of 1-Aminocyclopropane-1-Carboxylate (ACC) Deaminase Activity of <i>Sinorhizobium</i> sp. BL3 on Symbiosis with Mung Bean and Determinate Nodule Senescence. Microbes and Environments, 2015, 30, 310-320.	0.7	18
46	Characterization of Leaf Blade- and Leaf Sheath-Associated Bacterial Communities and Assessment of Their Responses to Environmental Changes in CO₂, Temperature, and Nitrogen Levels under Field Conditions. Microbes and Environments, 2015, 30, 51-62.	0.7	24
47	The Type III Secretion System (T3SS) is a Determinant for Rice-Endophyte Colonization by Non-Photosynthetic <i>Bradyrhizobium</i>. Microbes and Environments, 2015, 30, 291-300.	0.7	62
48	Genome Analysis of a Novel Bradyrhizobium sp. DOA9 Carrying a Symbiotic Plasmid. PLoS ONE, 2015, 10, e0117392.	1.1	52
49	Preferential Association of Endophytic Bradyrhizobia with Different Rice Cultivars and Its Implications for Rice Endophyte Evolution. Applied and Environmental Microbiology, 2015, 81, 3049-3061.	1.4	52
50	Elevated atmospheric CO2 levels affect community structure of rice root-associated bacteria. Frontiers in Microbiology, 2015, 6, 136.	1.5	38
51	Symbiosis Island Shuffling with Abundant Insertion Sequences in the Genomes of Extra-Slow-Growing Strains of Soybean Bradyrhizobia. Applied and Environmental Microbiology, 2015, 81, 4143-4154.	1.4	16
52	Peribacteroid solution of soybean root nodules partly induces genomic loci for differentiation into bacteroids of free-living Bradyrhizobium japonicum cells. Soil Science and Plant Nutrition, 2015, 61, 461-470.	0.8	4
53	Bacterial clade with the ribosomal RNA operon on a small plasmid rather than the chromosome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14343-14347.	3.3	47
54	Bacterial community shifts associated with high abundance of Rhizobium spp. in potato roots under macronutrient-deficient conditions. Soil Biology and Biochemistry, 2015, 80, 232-236.	4.2	10

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55	Metaproteomic Identification of Diazotrophic Methanotrophs and Their Localization in Root Tissues of Field-Grown Rice Plants. Applied and Environmental Microbiology, 2014, 80, 5043-5052.	1.4	101
56	The nitrateâ€sensing <scp>N</scp>as<scp>ST</scp> system regulates nitrous oxide reductase and periplasmic nitrate reductase in <scp><i>B</i></scp><i>radyrhizobium japonicum</i>. Environmental Microbiology, 2014, 16, 3263-3274.	1.8	19
57	A Rice Gene for Microbial Symbiosis, <i>Oryza sativa</i> <i>CCaMK</i> , Reduces CH ₄ Flux in a Paddy Field with Low Nitrogen Input. Applied and Environmental Microbiology, 2014, 80, 1995-2003.	1.4	39
58	Low Nitrogen Fertilization Adapts Rice Root Microbiome to Low Nutrient Environment by Changing Biogeochemical Functions. Microbes and Environments, 2014, 29, 50-59.	0.7	90
59	An Assessment of the Diversity of Culturable Bacteria from Main Root of Sugar Beet. Microbes and Environments, 2014, 29, 220-223.	0.7	17
60	Effects of Elevated Carbon Dioxide, Elevated Temperature, and Rice Growth Stage on the Community Structure of Rice Rootâ€“Associated Bacteria. Microbes and Environments, 2014, 29, 184-190.	0.7	41
61	Divergent <i>Nod</i>-Containing <i>Bradyrhizobium</i> sp. DOA9 with a Megaplasmid and its Host Range. Microbes and Environments, 2014, 29, 370-376.	0.7	22
62	Phylogeny and Functions of Bacterial Communities Associated with Field-Grown Rice Shoots. Microbes and Environments, 2014, 29, 329-332.	0.7	33
63	Relationship Between Soil Type and N₂O Reductase Genotype (<i>nosZ</i>) of Indigenous Soybean Bradyrhizobia: <i>nosZ</i>-minus Populations are Dominant in Andosols. Microbes and Environments, 2014, 29, 420-426.	0.7	32
64	Mitigation of nitrous oxide emissions from soils by Bradyrhizobium japonicum inoculation. Nature Climate Change, 2013, 3, 208-212.	8.1	117
65	Genome Analysis Suggests that the Soil Oligotrophic Bacterium Agromonas oligotrophica (Bradyrhizobium oligotrophicum) Is a Nitrogen-Fixing Symbiont of Aeschynomene indica. Applied and Environmental Microbiology, 2013, 79, 2542-2551.	1.4	49
66	Impact of <i>Azospirillum</i> sp. B510 Inoculation on Rice-Associated Bacterial Communities in a Paddy Field. Microbes and Environments, 2013, 28, 487-490.	0.7	29
67	Linked Expressions of <i>nap</i> and <i>nos</i> Genes in a Bradyrhizobium japonicum Mutant with Increased N ₂ O Reductase Activity. Applied and Environmental Microbiology, 2013, 79, 4178-4180.	1.4	10
68	The Type III Secretion System of Bradyrhizobium japonicum USDA122 Mediates Symbiotic Incompatibility with <i>Rj2</i> Soybean Plants. Applied and Environmental Microbiology, 2013, 79, 1048-1051.	1.4	71
69	Effects of Plant Genotype and Nitrogen Level on Bacterial Communities in Rice Shoots and Roots. Microbes and Environments, 2013, 28, 391-395.	0.7	34
70	Involvement of a Novel Genistein-Inducible Multidrug Efflux Pump of <i>Bradyrhizobium japonicum</i> Early in the Interaction with <i>Glycine max</i> (L.) Merr. Microbes and Environments, 2013, 28, 414-421.	0.7	16
71	Evolution of Bradyrhizobium-Aeschynomene Mutualism: Living Testimony of the Ancient World or Highly Evolved State?. Plant and Cell Physiology, 2012, 53, 2000-2007.	1.5	35
72	Pyrosequence Read Length of 16S rRNA Gene Affects Phylogenetic Assignment of Plant-associated Bacteria. Microbes and Environments, 2012, 27, 204-208.	0.7	19

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73	N₂O Emission from Degraded Soybean Nodules Depends on Denitrification by <i>Bradyrhizobium japonicum</i> and Other Microbes in the Rhizosphere. Microbes and Environments, 2012, 27, 470-476.	0.7	42
74	Complete Genome Sequence of <i>Bradyrhizobium</i> sp. S23321: Insights into Symbiosis Evolution in Soil Oligotrophs. Microbes and Environments, 2012, 27, 306-315.	0.7	76
75	Genetic Diversity, Symbiotic Evolution, and Proposed Infection Process of Bradyrhizobium Strains Isolated from Root Nodules of Aeschynomene americana L. in Thailand. Applied and Environmental Microbiology, 2012, 78, 6236-6250.	1.4	47
76	Complete Genome Sequence of the Soybean Symbiont Bradyrhizobium japonicum Strain USDA6T. Genes, 2011, 2, 763-787.	1.0	108
77	Isolation and Genetic Characterization of Aurantimonas and Methylobacterium Strains from Stems of Hypernodulated Soybeans. Microbes and Environments, 2011, 26, 172-180.	0.7	19
78	Identification of Mesorhizobium loti Genes Relevant to Symbiosis by Using Signature-Tagged Mutants. Microbes and Environments, 2011, 26, 165-171.	0.7	6
79	Nitrogen Cycling in Rice Paddy Environments: Past Achievements and Future Challenges. Microbes and Environments, 2011, 26, 282-292.	0.7	180
80	Nitrate-Dependent N ₂ O Emission from Intact Soybean Nodules via Denitrification by Bradyrhizobium japonicum Bacteroids. Applied and Environmental Microbiology, 2011, 77, 8787-8790.	1.4	27
81	Involvement of the SmeAB Multidrug Efflux Pump in Resistance to Plant Antimicrobials and Contribution to Nodulation Competitiveness in Sinorhizobium meliloti. Applied and Environmental Microbiology, 2011, 77, 2855-2862.	1.4	44
82	The Genotype of the Calcium/Calmodulin-Dependent Protein Kinase Gene (<i>CCaMK</i>) Determines Bacterial Community Diversity in Rice Roots under Paddy and Upland Field Conditions. Applied and Environmental Microbiology, 2011, 77, 4399-4405.	1.4	30
83	Autoregulation of Nodulation Interferes with Impacts of Nitrogen Fertilization Levels on the Leaf-Associated Bacterial Community in Soybeans. Applied and Environmental Microbiology, 2011, 77, 1973-1980.	1.4	50
84	The <i>cbbL</i> Gene is Required for Thiosulfate-Dependent Autotrophic Growth of <i>Bradyrhizobium japonicum</i>. Microbes and Environments, 2010, 25, 220-223.	0.7	20
85	Azospirillum sp. Strain B510 Enhances Rice Growth and Yield. Microbes and Environments, 2010, 25, 58-61.	0.7	69
86	Temperature-Dependent Expression of Type III Secretion System Genes and Its Regulation in <i>Bradyrhizobium japonicum</i>. Molecular Plant-Microbe Interactions, 2010, 23, 628-637.	1.4	10
87	Impact of plant genotype and nitrogen level on rice growth response to inoculation with<i>Azospirillum</i>sp. strain B510 under paddy field conditions. Soil Science and Plant Nutrition, 2010, 56, 636-644.	0.8	48
88	Identification of the Mesorhizobium loti gene responsible for glycerophosphorylation of periplasmic cyclic ÃŽÂ²-1,2-glucans. FEMS Microbiology Letters, 2010, 302, 131-137.	0.7	8
89	Community shifts of soybean stem-associated bacteria responding to different nodulation phenotypes and N levels. ISME Journal, 2010, 4, 315-326.	4.4	63
90	A Great Leap forward in Microbial Ecology. Microbes and Environments, 2010, 25, 230-240.	0.7	48

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91	Plant-Microbe Communications for Symbiosis. Plant and Cell Physiology, 2010, 51, 1377-1380.	1.5	67
92	Thiosulfate-Dependent Chemolithoautotrophic Growth of <i>Bradyrhizobium japonicum</i>. Applied and Environmental Microbiology, 2010, 76, 2402-2409.	1.4	41
93	Copper Metallochaperones are Required for the Assembly of Bacteroid Cytochrome c Oxidase Which is Functioning for Nitrogen Fixation in Soybean Nodules. Plant and Cell Physiology, 2010, 51, 1242-1246.	1.5	11
94	Complete Genomic Structure of the Cultivated Rice Endophyte Azospirillum sp. B510. DNA Research, 2010, 17, 37-50.	1.5	148
95	Community- and Genome-Based Views of Plant-Associated Bacteria: Plantâ€"Bacterial Interactions in Soybean and Rice. Plant and Cell Physiology, 2010, 51, 1398-1410.	1.5	118
96	Effects of Colonization of a Bacterial Endophyte,<i>Azospirillum</i>sp. B510, on Disease Resistance in Rice. Bioscience, Biotechnology and Biochemistry, 2009, 73, 2595-2599.	0.6	79
97	Aerobic Vanillate Degradation and C ₁ Compound Metabolism in <i>Bradyrhizobium japonicum</i>. Applied and Environmental Microbiology, 2009, 75, 5012-5017.	1.4	51
98	Molecular diversity of bacterial chitinases in arable soils and the effects of environmental factors on the chitinolytic bacterial community. Soil Biology and Biochemistry, 2009, 41, 473-480.	4.2	44
99	Development of a Bacterial Cell Enrichment Method and its Application to the Community Analysis in Soybean Stems. Microbial Ecology, 2009, 58, 703-714.	1.4	108
100	Genomic comparison of <i>Bradyrhizobium japonicum</i> strains with different symbiotic nitrogen-fixing capabilities and other Bradyrhizobiaceae members. ISME Journal, 2009, 3, 326-339.	4.4	67
101	The communities of endophytic diazotrophic bacteria in cultivated rice (Oryza sativa L.). Applied Soil Ecology, 2009, 42, 141-149.	2.1	101
102	Nitrous Oxide Emission and Microbial Community in the Rhizosphere of Nodulated Soybeans during the Late Growth Period. Microbes and Environments, 2009, 24, 64-67.	0.7	35
103	Nodulation-Dependent Communities of Culturable Bacterial Endophytes from Stems of Field-Grown Soybeans. Microbes and Environments, 2009, 24, 253-258.	0.7	32
104	Structural characterization of neutral and anionic glucans from Mesorhizobium loti. Carbohydrate Research, 2008, 343, 2422-2427.	1.1	19
105	Ethylene production in plants during transformation suppresses <i>vir</i> gene expression in <i>Agrobacterium tumefaciens</i>. New Phytologist, 2008, 178, 647-656.	3.5	59
106	Microbial Community Analysis of Field-Grown Soybeans with Different Nodulation Phenotypes. Applied and Environmental Microbiology, 2008, 74, 5704-5709.	1.4	39
107	1-Aminocyclopropane-1-Carboxylate Deaminase Enhances <i>Agrobacterium tumefaciens</i> -Mediated Gene Transfer into Plant Cells. Applied and Environmental Microbiology, 2008, 74, 2526-2528.	1.4	41
108	Generation of <i>Bradyrhizobium japonicum</i> Mutants with Increased N ₂ O Reductase Activity by Selection after Introduction of a Mutated <i>dnaQ</i> Gene. Applied and Environmental Microbiology, 2008, 74, 7258-7264.	1.4	28

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109	Soybean Seed Extracts Preferentially Express Genomic Loci of Bradyrhizobium japonicum in the Initial Interaction with Soybean, Glycine max (L.) Merr. DNA Research, 2008, 15, 201-214.	1.5	30
110	Construction of Signature-tagged Mutant Library in Mesorhizobium loti as a Powerful Tool for Functional Genomics. DNA Research, 2008, 15, 297-308.	1.5	41
111	NAD-Malic Enzyme Affects Nitrogen Fixing Activity of Bradyrhizobium japonicum USDA 110 Bacteroids in Soybean Nodules. Microbes and Environments, 2008, 23, 215-220.	0.7	14
112	Broad Distribution and Phylogeny of Anaerobic Endophytes of Cluster XIVa Clostridia in Plant Species Including Crops. Microbes and Environments, 2008, 23, 73-80.	0.7	23
113	A Mesorhizobium loti mutant with reduced glucan content shows defective invasion of its host plant Lotus japonicus. Microbiology (United Kingdom), 2007, 153, 3983-3993.	0.7	16
114	Rhizobitoxine-induced Chlorosis Occurs in Coincidence with Methionine Deficiency in Soybeans. Annals of Botany, 2007, 100, 55-59.	1.4	18
115	Analysis of Molecular Diversity of Bacterial Chitinase Genes in the Maize Rhizosphere Using Culture-Independent Methods. Microbes and Environments, 2007, 22, 71-77.	0.7	19
116	Microbial Diversity in Milled Rice as Revealed by Riosomal Intergenic Spacer Analysis. Microbes and Environments, 2007, 22, 165-174.	0.7	19
117	Microbial Community Analysis of the Phytosphere Using Culture-Independent Methodologies. Microbes and Environments, 2007, 22, 93-105.	0.7	52
118	Rhizobitoxine production inAgrobacterium tumefaciensC58 byBradyrhizobium elkanii rtxACDEFGgenes. FEMS Microbiology Letters, 2007, 269, 29-35.	0.7	11
119	Discrimination of the Commercial Seeds of Forage Crops using Ribosomal Intergenic Spacer Analysis. Breeding Science, 2006, 56, 185-188.	0.9	1
120	Community Analysis of Seed-Associated Microbes in Forage Crops using Culture-Independent Methods. Microbes and Environments, 2006, 21, 112-121.	0.7	22
121	Global Gene Expression in Bradyrhizobium japonicum Cultured with Vanillin, Vanillate, 4-Hydroxybenzoate and Protocatechuate. Microbes and Environments, 2006, 21, 240-250.	0.7	22
122	Correlation of Denitrifying Capability with the Existence of nap, nir, nor and nos Genes in Diverse Strains of Soybean Bradyrhizobia. Microbes and Environments, 2006, 21, 174-184.	0.7	40
123	Evaluation of the Nitrogen-fixing Ability of Endophytic Clostridia based on Acetylene Reduction and Reverse Transcription-PCR Targeting the nifH Transcript and Ribosomal RNA. Microbes and Environments, 2006, 21, 23-35.	0.7	21
124	Incorporation of a DNA Sequence Encoding Green Fluorescent Protein (GFP) into Endophytic Diazotroph from Sugarcane and Sweet Potato and the Colonizing Ability of these Bacteria in Brassica oleracea. Microbes and Environments, 2006, 21, 122-128.	0.7	15
125	Microbial Community Analysis in the Rhizosphere of a Transgenic Tomato that Overexpresses 3-Hydroxy-3-methylglutaryl Coenzyme A Reductase. Microbes and Environments, 2006, 21, 261-271.	0.7	16
126	Preferential nodulation of Glycine max, Glycine soja and Macroptilium atropurpureum by two Bradyrhizobium species japonicum and elkanii. FEMS Microbiology Ecology, 2006, 24, 49-56.	1.3	21

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127	A milestone for endophyte biotechnology. Nature Biotechnology, 2006, 24, 1357-1358.	9.4	8
128	Rhizobitoxine modulates plantâ€"microbe interactions by ethylene inhibition. Biotechnology Advances, 2006, 24, 382-388.	6.0	96
129	Symbiotic Bradyrhizobium japonicum Reduces N 2 O Surrounding the Soybean Root System via Nitrous Oxide Reductase. Applied and Environmental Microbiology, 2006, 72, 2526-2532.	1.4	56
130	Expression of the 1-Aminocyclopropane-1-Carboxylic Acid Deaminase Gene Requires Symbiotic Nitrogen-Fixing Regulator Gene nifA2 in Mesorhizobium loti MAFF303099. Applied and Environmental Microbiology, 2006, 72, 4964-4969.	1.4	94
131	Soil microbial community analysis in the environmental risk assessment of transgenic plants. Plant Biotechnology, 2006, 23, 137-151.	0.5	16
132	Effect of Inoculation with Anaerobic Nitrogen-Fixing Consortium on Salt Tolerance ofMiscanthus sinensis. Soil Science and Plant Nutrition, 2005, 51, 243-249.	0.8	39
133	Expression of the nifH Gene of a Herbaspirillum Endophyte in Wild Rice Species: Daily Rhythm during the Light-Dark Cycle. Applied and Environmental Microbiology, 2005, 71, 8183-8190.	1.4	56
134	Two Rhizobial Strains, Mesorhizobium loti MAFF303099 and Bradyrhizobium japonicum USDA110, Encode Haloalkane Dehalogenases with Novel Structures and Substrate Specificities. Applied and Environmental Microbiology, 2005, 71, 4372-4379.	1.4	73
135	Diazotrophic Endophytes in Rice: Colonization and Nitrogen Fixation of Herbaspirillum and Clostridium Species. , 2005, , 339-343.		1
136	Expression of a mutated melon ethylene receptor gene Cm-ETR1/H69A affects stamen development in Nicotiana tabacum. Plant Science, 2005, 169, 935-942.	1.7	37
137	Anaerobic Nitrogen-Fixing Consortia Consisting of Clostridia Isolated from Gramineous Plants. Applied and Environmental Microbiology, 2004, 70, 3096-3102.	1.4	84
138	Bradyrhizobium elkanii rtxC Gene Is Required for Expression of Symbiotic Phenotypes in the Final Step of Rhizobitoxine Biosynthesis. Applied and Environmental Microbiology, 2004, 70, 535-541.	1.4	29
139	New Method of Denitrification Analysis of Bradyrhizobium Field Isolates by Gas Chromatographic Determination of 15 N-Labeled N 2. Applied and Environmental Microbiology, 2004, 70, 2886-2891.	1.4	25
140	Transgenic Lotus japonicus with an Ethylene Receptor Gene Cm-ERS1/H70A Enhances Formation of Infection Threads and Nodule Primordia. Plant and Cell Physiology, 2004, 45, 427-435.	1.5	90
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