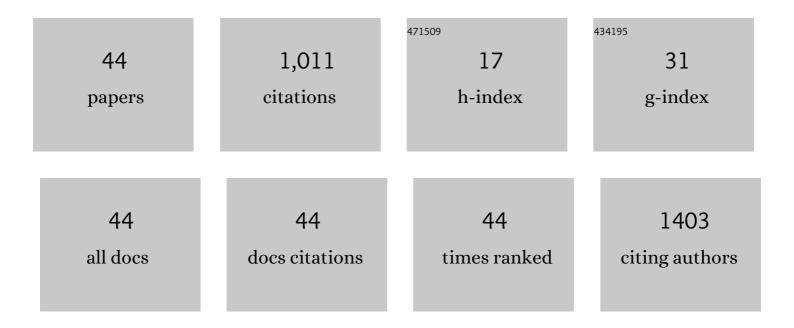
## Tomoyasu Nishizawa

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Higher diversity and abundance of denitrifying microorganisms in environments than considered previously. ISME Journal, 2015, 9, 1954-1965.	9.8	182
2	Detection of Betaproteobacteria inside the Mycelium of the Fungus Mortierella elongata. Microbes and Environments, 2010, 25, 321-324.	1.6	77
3	Mycoavidus cysteinexigens gen. nov., sp. nov., an endohyphal bacterium isolated from a soil isolate of the fungus Mortierella elongata. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2052-2057.	1.7	76
4	Phylogenetic and Functional Diversity of Denitrifying Bacteria Isolated from Various Rice Paddy and Rice-Soybean Rotation Fields. Microbes and Environments, 2011, 26, 30-35.	1.6	69
5	Draft Genome Sequence of the Betaproteobacterial Endosymbiont Associated with the Fungus <i>Mortierella elongata</i> FMR23-6. Genome Announcements, 2014, 2, .	0.8	46
6	Inoculation with N2-generating denitrifier strains mitigates N2O emission from agricultural soil fertilized with poultry manure. Biology and Fertility of Soils, 2014, 50, 1001-1007.	4.3	46
7	Analysis of Early Bacterial Communities on Volcanic Deposits on the Island of Miyake (Miyake-jima), Japan: a 6-year Study at a Fixed Site. Microbes and Environments, 2012, 27, 19-29.	1.6	41
8	Characterization of the locus of genes encoding enzymes producing heptadepsipeptide micropeptin in the unicellular cyanobacterium Microcystis. Journal of Biochemistry, 2011, 149, 475-485.	1.7	36
9	Cyclic heptapeptide microcystin biosynthesis requires the glutamate racemase gene. Microbiology (United Kingdom), 2001, 147, 1235-1241.	1.8	36
10	Complete Genome Sequence of Leptospirillum ferrooxidans Strain C2-3, Isolated from a Fresh Volcanic Ash Deposit on the Island of Miyake, Japan. Journal of Bacteriology, 2012, 194, 4122-4123.	2.2	34
11	Prevalence and Intra-Family Phylogenetic Divergence of <i>Burkholderiaceae</i> -Related Endobacteria Associated with Species of <i>Mortierella</i> . Microbes and Environments, 2018, 33, 417-427.	1.6	30
12	Complete Genome Sequence of the Denitrifying and N2O-Reducing Bacterium Azoarcus sp. Strain KH32C. Journal of Bacteriology, 2012, 194, 1255-1255.	2.2	29
13	Comparative Genomic Insights into Endofungal Lifestyles of Two Bacterial Endosymbionts, <i>Mycoavidus cysteinexigens</i> and <i>Burkholderia rhizoxinica</i> . Microbes and Environments, 2018, 33, 66-76.	1.6	28
14	Nitrous oxide (N2O)-reducing denitrifier-inoculated organic fertilizer mitigates N2O emissions from agricultural soils. Biology and Fertility of Soils, 2017, 53, 885-898.	4.3	26
15	Archaeal Diversity of Upland Rice Field Soils Assessed by the Terminal Restriction Fragment Length Polymorphism Method Combined with Real Time Quantitative-PCR and a Clone Library Analysis. Microbes and Environments, 2008, 23, 237-243.	1.6	23
16	Nitrogenase Activity (Acetylene Reduction) of an Iron-Oxidizing Leptospirillum Strain Cultured as a Pioneer Microbe from a Recent Volcanic Deposit on Miyake-Jima, Japan. Microbes and Environments, 2009, 24, 291-296.	1.6	22
17	Advantages of functional single-cell isolation method over standard agar plate dilution method as a tool for studying denitrifying bacteria in rice paddy soil. AMB Express, 2012, 2, 50.	3.0	19
18	Isolation and Molecular Characterization of a Multicellular Cyanobacterium, <i>Limnothrix/Pseudanabaena</i> sp. Strain ABRG5-3. Bioscience, Biotechnology and Biochemistry, 2010, 74, 1827-1835.	1.3	17

Tomoyasu Nishizawa

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19	In vivo and in vitro characterization of site-specific recombination of actinophage R4 integrase. Journal of General and Applied Microbiology, 2011, 57, 45-57.	0.7	17
20	Cloning and characterization of a new hetero-gene cluster of nonribosomal peptide synthetase and polyketide synthase from the cyanobacterium Microcystis aeruginosa K-139. Journal of General and Applied Microbiology, 2007, 53, 17-27.	0.7	13
21	Taxonomic composition of denitrifying bacterial isolates is different among three rice paddy field soils in Japan. Soil Science and Plant Nutrition, 2013, 59, 305-310.	1.9	13
22	Effects of <i>Rhizobium</i> Species Living with the Dark Septate Endophytic Fungus <i>Veronaeopsis simplex</i> on Organic Substrate Utilization by the Host. Microbes and Environments, 2018, 33, 102-106.	1.6	13
23	<i>Mycoavidus</i> sp. Strain B2-EB: Comparative Genomics Reveals Minimal Genomic Features Required by a Cultivable <i>Burkholderiaceae</i> -Related Endofungal Bacterium. Applied and Environmental Microbiology, 2020, 86, .	3.1	13
24	Complete genome sequence of Agrobacterium pusense VsBac-Y9, a bacterial symbiont of the dark septate endophytic fungus Veronaeopsis simplex Y34 with potential for improving fungal colonization in roots. Journal of Biotechnology, 2018, 284, 31-36.	3.8	12
25	Diversity within the Microcystin Biosynthetic Gene Clusters among the Genus Microcystis. Microbes and Environments, 2007, 22, 380-390.	1.6	11
26	Complete Genome Sequence of a Microcystin-Degrading Bacterium, Sphingosinicella microcystinivorans Strain B-9. Microbiology Resource Announcements, 2018, 7, .	0.6	11
27	Comparative Characterization of Bacterial Communities in Moss-Covered and Unvegetated Volcanic Deposits of Mount Merapi, Indonesia. Microbes and Environments, 2019, 34, 268-277.	1.6	9
28	<i>Azoarcus</i> sp. strain KH32C affects rice plant growth and the root-associated soil bacterial community in low nitrogen input paddy fields. Soil Science and Plant Nutrition, 2019, 65, 451-459.	1.9	8
29	Aposymbiosis of a <i>Burkholderiaceae</i> -Related Endobacterium Impacts on Sexual Reproduction of Its Fungal Host. Microbes and Environments, 2020, 35, n/a.	1.6	8
30	No Tillage Increases SOM in Labile Fraction but Not Stable Fraction of Andosols from a Long-Term Experiment in Japan. Agronomy, 2022, 12, 479.	3.0	7
31	Genome Sequence of Arthrobacter sp. UKPF54-2, a Plant Growth-Promoting Rhizobacterial Strain Isolated from Paddy Soil. Microbiology Resource Announcements, 2019, 8, .	0.6	6
32	Genome Sequences of Two Azospirillum sp. Strains, TSA2S and TSH100, Plant Growth-Promoting Rhizobacteria with N 2 O Mitigation Abilities. Microbiology Resource Announcements, 2019, 8, .	0.6	6
33	FVIIa-sTF and Thrombin Inhibitory Activities of Compounds Isolated from Microcystis aeruginosa K-139. Marine Drugs, 2017, 15, 275.	4.6	5
34	Complete Genome Sequence of the Nonheterocystous Cyanobacterium <i>Pseudanabaena</i> sp. ABRG5-3. Genome Announcements, 2018, 6, .	0.8	4
35	Construction of a stepwise gene integration system by transient expression of actinophage R4 integrase in cyanobacterium Synechocystis sp. PCC 6803. Molecular Genetics and Genomics, 2014, 289, 615-623.	2.1	3
36	Comparative Analysis of the Genetic Basis of Branched Nonylphenol Degradation by <i>Sphingobium amiense</i> DSM 16289 <sup>T</sup> and <i>Sphingobium cloacae</i> JCM 10874 <sup>T</sup> . Microbes and Environments, 2018, 33, 450-454.	1.6	3

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37	Whole-Genome Sequence of Entomortierella parvispora E1425, a Mucoromycotan Fungus Associated with <i>Burkholderiaceae</i> -Related Endosymbiotic Bacteria. Microbiology Resource Announcements, 2022, 11, e0110121.	0.6	3
38	Complete Genome Sequence of the Nonylphenol-Degrading Bacterium Sphingobium cloacae JCM 10874 <sup>T</sup> . Genome Announcements, 2016, 4, .	0.8	2
39	Complete Genome Sequence of Streptomyces parvulus 2297, Integrating Site-Specifically with Actinophage R4. Genome Announcements, 2016, 4, .	0.8	2
40	Root bacteriome of a pioneer grass Miscanthus condensatus along restored vegetation on recent Miyake-jima volcanic deposits. Rhizosphere, 2021, 19, 100422.	3.0	2
41	Actinophage R4 integraseâ€based siteâ€specific chromosomal integration of nonâ€replicative closed circular DNA. Journal of Basic Microbiology, 2016, 56, 635-644.	3.3	1
42	Molecular Analysis of the Cyanobacterial Community in Gastric Contents of Egrets with Symptoms of Steatitis. Open Microbiology Journal, 2015, 9, 160-166.	0.7	1
43	Genome Sequence of Novoherbaspirillum sp. UKPF54, a Plant Growth-Promoting Rhizobacterial Strain with N 2 O-Mitigating Abilities, Isolated from Paddy Soil. Microbiology Resource Announcements, 2020, 9, .	0.6	1
44	Complete Genome Sequence of a Chemolithoautotrophic Iron-Oxidizing Bacterium, Acidithiobacillus ferrooxidans Strain NFP31, Isolated from Volcanic Ash Deposits on Miyake-Jima, Japan. Microbiology Resource Announcements, 2022, 11, e0100621.	0.6	0