Shin Haruta

List of Publications by Year
in descending order

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85

papers

4,157

citations

117625

34

h-index

114465

63

g-index

86

all docs

86

docs citations

86

times ranked

4150

citing authors

#	Article	IF	Citations
1	Neotabrizicola shimadae gen. nov., sp. nov., an aerobic anoxygenic phototrophic bacterium harbouring photosynthetic genes in the family Rhodobacteraceae, isolated from a terrestrial hot spring. Antonie Van Leeuwenhoek, 2022, 115, 731-740.	1.7	8
2	Hydrogenophilus thiooxidans sp. nov., a moderately thermophilic chemotrophic bacterium unable to grow on hydrogen gas, isolated from hot spring microbial mats. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	6
3	Nitrogen-fixing Ability and Nitrogen Fixation-related Genes of Thermophilic Fermentative Bacteria in the Genus <i>Caldicellulosiruptor</i>. Microbes and Environments, 2021, 36, n/a.	1.6	15
4	In-Situ Metatranscriptomic Analyses Reveal the Metabolic Flexibility of the Thermophilic Anoxygenic Photosynthetic Bacterium Chloroflexus aggregans in a Hot Spring Cyanobacteria-Dominated Microbial Mat. Microorganisms, 2021, 9, 652.	3.6	12
5	Caldicellulosiruptor diazotrophicus sp. nov., a thermophilic, nitrogen-fixing fermentative bacterium isolated from a terrestrial hot spring in Japan. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	6
6	Metagenome-Assembled Genome Sequences Recovered from Epilithic River Biofilm in the Tama River, Japan. Microbiology Resource Announcements, 2021, 10, e0066421.	0.6	1
7	Aerobic Production of Bacteriochlorophylls in the Filamentous Anoxygenic Photosynthetic Bacterium, <i>Chloroflexus aurantiacus</i> in the Light. Microbes and Environments, 2020, 35, n/a.	1.6	2
8	Tree of motility â€“ A proposed history of motility systems in the tree of life. Genes To Cells, 2020, 25, 6-21.	1.2	108
9	Aquabacterium pictum sp. nov., the first aerobic bacteriochlorophyll a-containing fresh water bacterium in the genus Aquabacterium of the class Betaproteobacteria. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 596-603.	1.7	15
10	Thermaurantimonas aggregans gen. nov., sp. nov., a moderately thermophilic heterotrophic aggregating bacterium isolated from microbial mats at a terrestrial hot spring. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 1117-1121.	1.7	11
11	Hydrogen-dependent autotrophic growth in phototrophic and chemolithotrophic cultures of thermophilic bacteria, <i>Chloroflexus aggregans</i> and <i>Chloroflexus aurantiacus</i>, isolated from Nakabusa hot springs. FEMS Microbiology Letters, 2019, 366, .	1.8	12
12	Minimal Interspecies Interaction Adjustment (MIIA): Inference of Neighbor-Dependent Interactions in Microbial Communities. Frontiers in Microbiology, 2019, 10, 1264.	3.5	12
13	Symbiotic Growth of a Thermophilic Sulfide-Oxidizing Photoautotroph and an Elemental Sulfur-Disproportionating Chemolithoautotroph and Cooperative Dissimilatory Oxidation of Sulfide to Sulfate. Frontiers in Microbiology, 2019, 10, 1150.	3.5	9
14	Sulfide-dependent Photoautotrophy in the Filamentous Anoxygenic Phototrophic Bacterium, <i>Chloroflexus aggregans</i>. Microbes and Environments, 2019, 34, 304-309.	1.6	9
15	Prediction of Neighbor-Dependent Microbial Interactions From Limited Population Data. Frontiers in Microbiology, 2019, 10, 3049.	3.5	8
16	Nitrite-reducing ability is related to growth inhibition by nitrite in Rhodobacter sphaeroides f. sp. denitrificans. Bioscience, Biotechnology and Biochemistry, 2018, 82, 148-151.	1.3	1
17	Nitrogenase Activity in Thermophilic Chemolithoautotrophic Bacteria in the Phylum <i>Aquificae</i> Isolated under Nitrogen-Fixing Conditions from Nakabusa Hot Springs. Microbes and Environments, 2018, 33, 394-401.	1.6	21
18	Phylogenetic Diversity of Nitrogenase Reductase Genes and Possible Nitrogen-Fixing Bacteria in Thermophilic Chemosynthetic Microbial Communities in Nakabusa Hot Springs. Microbes and Environments, 2018, 33, 357-365.	1.6	25

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19	Model Microbial Consortia as Tools for Understanding Complex Microbial Communities. Current Genomics, 2018, 19, 723-733.	1.6	22
20	Increase of Salt Tolerance in Carbon-Starved Cells of Rhodopseudomonas palustris Depending on Photosynthesis or Respiration. Microorganisms, 2018, 6, 4.	3.6	6
21	Different Metabolomic Responses to Carbon Starvation between Light and Dark Conditions in the Purple Photosynthetic Bacterium, <i>Rhodopseudomonas palustris</i>. Microbes and Environments, 2018, 33, 83-88.	1.6	6
22	Nitrogen Fixation in Thermophilic Chemosynthetic Microbial Communities Depending on Hydrogen, Sulfate, and Carbon Dioxide. Microbes and Environments, 2018, 33, 10-18.	1.6	30
23	Ca²⁺ in Hybridization Solutions for Fluorescence <i>in situ</i> Hybridization Facilitates the Detection of <i>Enterobacteriaceae</i>. Microbes and Environments, 2017, 32, 142-146.	1.6	3
24	Editorial: Development of Microbial Ecological Theory: Stability, Plasticity, and Evolution of Microbial Ecosystems. Frontiers in Microbiology, 2016, 7, 2069.	3.5	5
25	Phylogenetically Diverse Aerobic Anoxygenic Phototrophic Bacteria Isolated from Epilithic Biofilms in Tama River, Japan. Microbes and Environments, 2016, 31, 299-306.	1.6	23
26	Gliding motility driven by individual cell-surface movements in a multicellular filamentous bacterium<i>Chloroflexus aggregans</i>. FEMS Microbiology Letters, 2016, 363, fnw056.	1.8	11
27	Survivability of Microbes in Natural Environments and Their Ecological Impacts. Microbes and Environments, 2015, 30, 123-125.	1.6	59
28	Secreted protease mediates interspecies interaction and promotes cell aggregation of the photosynthetic bacterium Chloroflexus aggregans. FEMS Microbiology Letters, 2015, 362, 1-5.	1.8	7
29	Reorganization of the bacterial and archaeal populations associated with organic loading conditions in a thermophilic anaerobic digester. Journal of Bioscience and Bioengineering, 2015, 119, 337-344.	2.2	22
30	Involvement of a novel fermentative bacterium in acidification in a thermophilic anaerobic digester. FEMS Microbiology Letters, 2014, 361, 62-67.	1.8	4
31	Genome Sequence of the Thermophilic Cyanobacterium <i>Thermosynechococcus</i> sp. Strain NK55a. Genome Announcements, 2014, 2, .	0.8	20
32	Differences in Survivability under Starvation Conditions Among Four Species of Purple Nonsulfur Phototrophic Bacteria. Microbes and Environments, 2014, 29, 326-328.	1.6	9
33	Rediscovery of the Microbial World in Microbial Ecology. Microbes and Environments, 2013, 28, 281-284.	1.6	2
34	<i>Candidatus</i> Methanogranum caenicola: a Novel Methanogen from the Anaerobic Digested Sludge, and Proposal of <i>Methanomassiliicoccaceae</i> fam. nov. and <i>Methanomassiliicoccales</i> ord. nov., for a Methanogenic Lineage of the Class <i>Thermoplasmata</i>. Microbes and Environments, 2013, 28, 244-250.	1.6	211
35	Challenges for Complex Microbial Ecosystems: Combination of Experimental Approaches with Mathematical Modeling. Microbes and Environments, 2013, 28, 285-294.	1.6	19
36	Production and Consumption of Hydrogen in Hot Spring Microbial Mats Dominated by a Filamentous Anoxygenic Photosynthetic Bacterium. Microbes and Environments, 2012, 27, 293-299.	1.6	67

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37	Diversification of Bacterial Community Composition along a Temperature Gradient at a Thermal Spring. Microbes and Environments, 2012, 27, 374-381.	1.6	87
38	Complete Genome Sequence of <i>Bradyrhizobium</i> sp. S23321: Insights into Symbiosis Evolution in Soil Oligotrophs. Microbes and Environments, 2012, 27, 306-315.	1.6	76
39	Diversity of Purple Phototrophic Bacteria, Inferred from <i>pufM</i> Gene, within Epilithic Biofilm in Tama River, Japan. Microbes and Environments, 2012, 27, 327-329.	1.6	11
40	Methanogenic pathway and community structure in a thermophilic anaerobic digestion process of organic solid waste. Journal of Bioscience and Bioengineering, 2011, 111, 41-46.	2.2	124
41	Distinctive Responses of Metabolically Active Microbiota to Acidification in a Thermophilic Anaerobic Digester. Microbial Ecology, 2011, 61, 595-605.	2.8	81
42	Detection of active, potentially acetate-oxidizing syntrophs in an anaerobic digester by flux measurement and formyltetrahydrofolate synthetase (FTHFS) expression profiling. Microbiology (United Kingdom), 2011, 157, 1980-1989.	1.8	58
43	Determinative Factors of Competitive Advantage between Aerobic Bacteria for Niches at the Air-Liquid Interface. Microbes and Environments, 2010, 25, 317-320.	1.6	19
44	Bacterial community dynamics during reduction of odorous compounds in aerated pig manure slurry. Journal of Applied Microbiology, 2009, 106, 118-129.	3.1	22
45	Intertwined interspecies relationships: approaches to untangle the microbial network. Environmental Microbiology, 2009, 11, 2963-2969.	3.8	66
46	Traditional Pot Fermentation of Rice Vinegar-from the Viewpoint of Microbiology-. Journal of the Brewing Society of Japan, 2009, 104, 652-657.	0.3	0
47	Network Relationships of Bacteria in a Stable Mixed Culture. Microbial Ecology, 2008, 56, 403-411.	2.8	81
48	Coexistence of Antibiotic-Producing and Antibiotic-Sensitive Bacteria in Biofilms Is Mediated by Resistant Bacteria. Applied and Environmental Microbiology, 2008, 74, 3887-3894.	3.1	86
49	Effect of Adding Cellulolytic Bacterium on Stable Cellulose-Degrading Microbial Community. Journal of Bioscience and Bioengineering, 2007, 104, 432-434.	2.2	11
50	Microbial population in the biomass adhering to supporting material in a packed-bed reactor degrading organic solid waste. Applied Microbiology and Biotechnology, 2007, 75, 941-952.	3.6	59
51	Dynamic Transition of a Methanogenic Population in Response to the Concentration of Volatile Fatty Acids in a Thermophilic Anaerobic Digester. Applied and Environmental Microbiology, 2006, 72, 1623-1630.	3.1	281
52	Microbial community in methanogenic packed-bed reactor successfully operating at short hydraulic retention time. Journal of Bioscience and Bioengineering, 2006, 101, 271-273.	2.2	17
53	Archaeal population on supporting material in methanogenic packed-bed reactor. Journal of Bioscience and Bioengineering, 2006, 102, 244-246.	2.2	15
54	Direct comparison of single-strand conformation polymorphism (SSCP) and denaturing gradient gel electrophoresis (DGGE) to characterize a microbial community on the basis of 16S rRNA gene fragments. Journal of Microbiological Methods, 2006, 66, 165-169.	1.6	40

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55	Diversity of a stable enrichment culture which is useful for silage inoculant and its succession in alfalfa silage. FEMS Microbiology Ecology, 2006, 57, 106-115.	2.7	75
56	Changes in bacterial community during fermentative hydrogen and acid production from organic waste by thermophilic anaerobic microflora. Journal of Applied Microbiology, 2006, 101, 331-343.	3.1	84
57	Succession of bacterial and fungal communities during a traditional pot fermentation of rice vinegar assessed by PCR-mediated denaturing gradient gel electrophoresis. International Journal of Food Microbiology, 2006, 109, 79-87.	4.7	178
58	Microbial diversity in biodegradation and reutilization processes of garbage. Journal of Bioscience and Bioengineering, 2005, 99, 1-11.	2.2	48
59	Stable Coexistence of Five Bacterial Strains as a Cellulose-Degrading Community. Applied and Environmental Microbiology, 2005, 71, 7099-7106.	3.1	239
60	Enzyme Production-Based Approach for Determining the Functions of Microorganisms within a Community. Applied and Environmental Microbiology, 2004, 70, 3329-3337.	3.1	23
61	Clostridium straminisolvens sp. nov., a moderately thermophilic, aerotolerant and cellulolytic bacterium isolated from a cellulose-degrading bacterial community. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 2043-2047.	1.7	108
62	Succession of a microbial community during stable operation of a semi-continuous garbage-decomposing system. Journal of Bioscience and Bioengineering, 2004, 98, 20-27.	2.2	17
63	Effective cellulose degradation by a mixed-culture system composed of a cellulolytic Clostridium and aerobic non-cellulolytic bacteria. FEMS Microbiology Ecology, 2004, 51, 133-142.	2.7	163
64	Cerasibacillus quisquiliarum gen. nov., sp. nov., isolated from a semi-continuous decomposing system of kitchen refuse. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 1063-1069.	1.7	42
65	Isolation and characterization of predominant microorganisms during decomposition of waste materials in a field-scale composter. Journal of Bioscience and Bioengineering, 2003, 95, 368-373.	2.2	32
66	è‡é›‘å¾®ç”Ÿç‰©ç³»ã®è§£æžã¨ã®åˆ©ç”¨. Nippon Nogeikagaku Kaishi, 2002, 76, 724-726.	0.0	0
67	Construction of a stable microbial community with high cellulose-degradation ability. Applied Microbiology and Biotechnology, 2002, 59, 529-534.	3.6	200
68	Microbial community changes during organic solid waste treatment analyzed by double gradient-denaturing gradient gel electrophoresis and fluorescence in situ hybridization. Applied Microbiology and Biotechnology, 2002, 60, 224-231.	3.6	68
69	Characterization of an Extendedâ€Spectrum Class C Î²â€Lactamase of <i>Citrobacter freundii</i>. Microbiology and Immunology, 2001, 45, 277-283.	1.4	2
70	Changes in product formation and bacterial community by dilution rate on carbohydrate fermentation by methanogenic microflora in continuous flow stirred tank reactor. Applied Microbiology and Biotechnology, 2001, 57, 65-73.	3.6	65
71	Microbial community in anaerobic hydrogen-producing microflora enriched from sludge compost. Applied Microbiology and Biotechnology, 2001, 57, 555-562.	3.6	235
72	Characterization of the active-site residues asparagine 167 and lysine 161 of the IMP-1 metallo ÃŽÂ²-lactamase. FEMS Microbiology Letters, 2001, 197, 85-89.	1.8	26

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73	Denaturing gradient gel electrophoresis analyses of microbial community from field-scale composter. Journal of Bioscience and Bioengineering, 2001, 91, 159-165.	2.2	91
74	Characterization of a microorganism isolated from the effluent of hydrogen fermentation by microflora. Journal of Bioscience and Bioengineering, 2001, 92, 397-400.	2.2	75
75	Analyses of microbial community within a composter operated using household garbage with special reference to the addition of soybean oil. Journal of Bioscience and Bioengineering, 2001, 91, 456-461.	2.2	31
76	Denaturing Gradient Gel Electrophoresis Analyses of Microbial Community from Field-Scale Composter.. Journal of Bioscience and Bioengineering, 2001, 91, 159-165.	2.2	58
77	Analyses of Microbial Community within a Composter Operated Using Household Garbage with Special Reference to the Addition of Soybean Oil.. Journal of Bioscience and Bioengineering, 2001, 91, 456-461.	2.2	18
78	Characterization of a Microorganism Isolated from the Effluent of Hydrogen Fermentation by Microflora.. Journal of Bioscience and Bioengineering, 2001, 92, 397-400.	2.2	20
79	Functional Analysis of the Active Site of a Metallo-Î²-Lactamase Proliferating in Japan. Antimicrobial Agents and Chemotherapy, 2000, 44, 2304-2309.	3.2	53
80	Amino Acid Substitutions in a Variant of IMP-1 Metallo-Î²-Lactamase. Antimicrobial Agents and Chemotherapy, 2000, 44, 2023-2027.	3.2	108
81	Novel metallo ÃŽÂ²-lactamase mediated by aShigella flexneriplasmid. FEMS Microbiology Letters, 1998, 162, 201-206.	1.8	37
82	Novel metallo Î²-lactamase mediated by a Shigella flexneri plasmid. FEMS Microbiology Letters, 1998, 162, 201-206.	1.8	29
83	Resistance to Oxyimino Î²â€Łactams Due to a Mutation of Chromosomal Î²â€Łactamase in <i>Citrobacter freundii</i>. Microbiology and Immunology, 1998, 42, 165-169.	1.4	7
84	Molecular Evolution of a Class C Î²-Lactamase Extending Its Substrate Specificity. Journal of Biological Chemistry, 1995, 270, 5729-5735.	3.4	76
85	Molecular evolution of a class C Î²-lactamase extending its substrate specificity.. Journal of Biological Chemistry, 1995, 270, 21428.	3.4	8