Shin Haruta

List of Publications by Year in descending order

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117625 114465 4,157 85 34 63 citations h-index g-index papers 86 86 86 4150 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	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
2	Stable Coexistence of Five Bacterial Strains as a Cellulose-Degrading Community. Applied and Environmental Microbiology, 2005, 71, 7099-7106.	3.1	239
3	Microbial community in anaerobic hydrogen-producing microflora enriched from sludge compost. Applied Microbiology and Biotechnology, 2001, 57, 555-562.	3.6	235
4	<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
5	Construction of a stable microbial community with high cellulose-degradation ability. Applied Microbiology and Biotechnology, 2002, 59, 529-534.	3.6	200
6	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
7	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
8	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
9	Amino Acid Substitutions in a Variant of IMP-1 Metallo- \hat{l}^2 -Lactamase. Antimicrobial Agents and Chemotherapy, 2000, 44, 2023-2027.	3.2	108
10	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
11	Tree of motility – A proposed history of motility systems in the tree of life. Genes To Cells, 2020, 25, 6-21.	1.2	108
12	Denaturing gradient gel electrophoresis analyses of microbial community from field-scale composter. Journal of Bioscience and Bioengineering, 2001, 91, 159-165.	2.2	91
13	Diversification of Bacterial Community Composition along a Temperature Gradient at a Thermal Spring. Microbes and Environments, 2012, 27, 374-381.	1.6	87
14	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
15	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
16	Network Relationships of Bacteria in a Stable Mixed Culture. Microbial Ecology, 2008, 56, 403-411.	2.8	81
17	Distinctive Responses of Metabolically Active Microbiota to Acidification in a Thermophilic Anaerobic Digester. Microbial Ecology, 2011, 61, 595-605.	2.8	81
18	Molecular Evolution of a Class C \hat{l}^2 -Lactamase Extending Its Substrate Specificity. Journal of Biological Chemistry, 1995, 270, 5729-5735.	3.4	76

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19	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
20	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
21	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
22	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
23	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
24	Intertwined interspecies relationships: approaches to untangle the microbial network. Environmental Microbiology, 2009, 11, 2963-2969.	3.8	66
25	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
26	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
27	Survivability of Microbes in Natural Environments and Their Ecological Impacts. Microbes and Environments, 2015, 30, 123-125.	1.6	59
28	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
29	Denaturing Gradient Gel Electrophoresis Analyses of Microbial Community from Field-Scale Composter Journal of Bioscience and Bioengineering, 2001, 91, 159-165.	2.2	58
30	Functional Analysis of the Active Site of a Metallo- \hat{l}^2 -Lactamase Proliferating in Japan. Antimicrobial Agents and Chemotherapy, 2000, 44, 2304-2309.	3.2	53
31	Microbial diversity in biodegradation and reutilization processes of garbage. Journal of Bioscience and Bioengineering, 2005, 99, 1-11.	2.2	48
32	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
33	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
34	Novel metallo β-lactamase mediated by aShigella flexneriplasmid. FEMS Microbiology Letters, 1998, 162, 201-206.	1.8	37
35	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
36	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

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37	Nitrogen Fixation in Thermophilic Chemosynthetic Microbial Communities Depending on Hydrogen, Sulfate, and Carbon Dioxide. Microbes and Environments, 2018, 33, 10-18.	1.6	30
38	Novel metallo \hat{I}^2 -lactamase mediated by a Shigella flexneri plasmid. FEMS Microbiology Letters, 1998, 162, 201-206.	1.8	29
39	Characterization of the active-site residues asparagine 167 and lysine 161 of the IMP-1 metallo $\tilde{A}\check{Z}\hat{A}^2$ -lactamase. FEMS Microbiology Letters, 2001, 197, 85-89.	1.8	26
40	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
41	Enzyme Production-Based Approach for Determining the Functions of Microorganisms within a Community. Applied and Environmental Microbiology, 2004, 70, 3329-3337.	3.1	23
42	Phylogenetically Diverse Aerobic Anoxygenic Phototrophic Bacteria Isolated from Epilithic Biofilms in Tama River, Japan. Microbes and Environments, 2016, 31, 299-306.	1.6	23
43	Bacterial community dynamics during reduction of odorous compounds in aerated pig manure slurry. Journal of Applied Microbiology, 2009, 106, 118-129.	3.1	22
44	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
45	Model Microbial Consortia as Tools for Understanding Complex Microbial Communities. Current Genomics, 2018, 19, 723-733.	1.6	22
46	Nitrogenase Activity in Thermophilic Chemolithoautotrophic Bacteria in the Phylum & lt;i>Aquificae Isolated under Nitrogen-Fixing Conditions from Nakabusa Hot Springs. Microbes and Environments, 2018, 33, 394-401.	1.6	21
47	Genome Sequence of the Thermophilic Cyanobacterium <i>Thermosynechococcus</i> sp. Strain NK55a. Genome Announcements, 2014, 2, .	0.8	20
48	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
49	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
50	Challenges for Complex Microbial Ecosystems: Combination of Experimental Approaches with Mathematical Modeling. Microbes and Environments, 2013, 28, 285-294.	1.6	19
51	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
52	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
53	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
54	Archaeal population on supporting material in methanogenic packed-bed reactor. Journal of Bioscience and Bioengineering, 2006, 102, 244-246.	2.2	15

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55	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
56	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
57	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
58	Minimal Interspecies Interaction Adjustment (MIIA): Inference of Neighbor-Dependent Interactions in Microbial Communities. Frontiers in Microbiology, 2019, 10, 1264.	3. 5	12
59	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
60	Effect of Adding Cellulolytic Bacterium on Stable Cellulose-Degrading Microbial Community. Journal of Bioscience and Bioengineering, 2007, 104, 432-434.	2.2	11
61	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
62	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
63	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
64	Differences in Survivability under Starvation Conditions Among Four Species of Purple Nonsulfur Phototrophic Bacteria. Microbes and Environments, 2014, 29, 326-328.	1.6	9
65	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
66	Sulfide-dependent Photoautotrophy in the Filamentous Anoxygenic Phototrophic Bacterium, <i>Chloroflexus aggregans</i> . Microbes and Environments, 2019, 34, 304-309.	1.6	9
67	Molecular evolution of a class C \hat{l}^2 -lactamase extending its substrate specificity Journal of Biological Chemistry, 1995, 270, 21428.	3.4	8
68	Prediction of Neighbor-Dependent Microbial Interactions From Limited Population Data. Frontiers in Microbiology, 2019, 10, 3049.	3.5	8
69	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
70	Resistance to Oxyimino βâ€Lactams Due to a Mutation of Chromosomal βâ€Lactamase in <i>Citrobacter freundii</i> . Microbiology and Immunology, 1998, 42, 165-169.	1.4	7
71	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
72	Increase of Salt Tolerance in Carbon-Starved Cells of Rhodopseudomonas palustris Depending on Photosynthesis or Respiration. Microorganisms, 2018, 6, 4.	3.6	6

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73	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
74	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
75	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
76	Editorial: Development of Microbial Ecological Theory: Stability, Plasticity, and Evolution of Microbial Ecosystems. Frontiers in Microbiology, 2016, 7, 2069.	3.5	5
77	Involvement of a novel fermentative bacterium in acidification in a thermophilic anaerobic digester. FEMS Microbiology Letters, 2014, 361, 62-67.	1.8	4
78	Ca ²⁺ in Hybridization Solutions for Fluorescence <i>in situ</i> the Detection of <i>Enterobacteriaceae</i> Microbes and Environments, 2017, 32, 142-146.	1.6	3
79	Characterization of an Extendedâ€Spectrum Class C βâ€Lactamase of <i>Citrobacter freundii</i> i>. Microbiology and Immunology, 2001, 45, 277-283.	1.4	2
80	Rediscovery of the Microbial World in Microbial Ecology. Microbes and Environments, 2013, 28, 281-284.	1.6	2
81	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
82	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
83	Metagenome-Assembled Genome Sequences Recovered from Epilithic River Biofilm in the Tama River, Japan. Microbiology Resource Announcements, 2021, 10, e0066421.	0.6	1
84	è‡é›'微生物系ã®è§£æžãëãã®å^©ç"". Nippon Nogeikagaku Kaishi, 2002, 76, 724-726.	0.0	0
85	Traditional Pot Fermentation of Rice Vinegar-from the Viewpoint of Microbiology Journal of the Brewing Society of Japan, 2009, 104, 652-657.	0.3	o