

Yuji Sekiguchi

List of Publications by Year in descending order

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117
papers

8,981
citations

47006

47
h-index

42399

92
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all docs

133
docs citations

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times ranked

8406
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization and Demonstration of Mock Communities as Control Reagents for Accurate Human Microbiome Community Measurements. <i>Microbiology Spectrum</i> , 2022, 10, e0191521.	3.0	17
2	Validation and standardization of DNA extraction and library construction methods for metagenomics-based human fecal microbiome measurements. <i>Microbiome</i> , 2021, 9, 95.	11.1	37
3	Sequence-Specific Capture of Oligonucleotide Probes (SCOPE): a Simple and Rapid Microbial rRNA Quantification Method Using a Molecular Weight Cutoff Membrane. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0116721.	3.1	0
4	Genomic and Physiological Characteristics of a Novel Nitrite-Oxidizing <i>Nitrospira</i> Strain Isolated From a Drinking Water Treatment Plant. <i>Frontiers in Microbiology</i> , 2020, 11, 545190.	3.5	12
5	Complete Genome Sequence of <i>Collinsella aerofaciens</i> JCM 10188. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
6	Physiological and genomic characterization of a new <i>Candidatus Nitrotoga</i> isolate. <i>Environmental Microbiology</i> , 2020, 22, 2365-2382.	3.8	26
7	Complete Genome Sequence of <i>Blautia producta</i> JCM 1471 T. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
8	Complete Genome Sequence of <i>Megamonas funiformis</i> JCM 14723 T. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2
9	Complete Genome Sequence of <i>Flavonifractor plautii</i> JCM 32125 T. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
10	Diversity and geochemical community assembly processes of the living rare biosphere in a sand-and-gravel aquifer ecosystem in the Midwestern United States. <i>Scientific Reports</i> , 2019, 9, 13484.	3.3	14
11	Genome Features and Secondary Metabolites Biosynthetic Potential of the Class <i>Ktedonobacteria</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 893.	3.5	61
12	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. <i>Scientific Reports</i> , 2018, 8, 8128.	3.3	11
13	Sample tracking in microbiome community profiling assays using synthetic 16S rRNA gene spike-in controls. <i>Scientific Reports</i> , 2018, 8, 9095.	3.3	17
14	Synthetic spike-in standards for high-throughput 16S rRNA gene amplicon sequencing. <i>Nucleic Acids Research</i> , 2017, 45, gkw984.	14.5	135
15	Four Aromatic Sulfates with an Inhibitory Effect against HCV NS3 Helicase from the Crinoid <i>Alloeocomatella polycladia</i> . <i>Marine Drugs</i> , 2017, 15, 117.	4.6	6
16	Draft Genome Sequence of <i>Terrimicrobium sacchariphilum</i> NM-5, a Facultative Anaerobic Soil Bacterium of the Class <i>Spartobacteria</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	4
17	Draft Genome Sequence of <i>Paludibacter jiangxiensis</i> NM7, a Propionate-Producing Fermentative Bacterium. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
18	Genomic Analysis of Two Phylogenetically Distinct <i>Nitrospira</i> Species Reveals Their Genomic Plasticity and Functional Diversity. <i>Frontiers in Microbiology</i> , 2017, 8, 2637.	3.5	40

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19	Microbial community structure of methanogenic benzene-degrading cultures enriched from five different sediments. <i>Journal of General and Applied Microbiology</i> , 2016, 62, 266-271.	0.7	1
20	Ecophysiology and Comparative Genomics of <i>Nitrosomonas mobilis</i> Ms1 Isolated from Autotrophic Nitrifying Granules of Wastewater Treatment Bioreactor. <i>Frontiers in Microbiology</i> , 2016, 7, 1869.	3.5	26
21	Comparative Genomics of Syntrophic Branched-Chain Fatty Acid Degrading Bacteria. <i>Microbes and Environments</i> , 2016, 31, 288-292.	1.6	19
22	Draft Genome Sequence of the Syntrophic Lactate-Degrading Bacterium <i>Tepidanaerobacter syntrophicus</i> JL ^T . <i>Genome Announcements</i> , 2016, 4, .	0.8	4
23	Draft Genome Sequence of <i>Thermodesulfovibrio aggregans</i> TGE-P1 T , an Obligately Anaerobic, Thermophilic, Sulfate-Reducing Bacterium in the Phylum Nitrospirae. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
24	Comparative Genomics of Candidate Phylum TM6 Suggests That Parasitism Is Widespread and Ancestral in This Lineage. <i>Molecular Biology and Evolution</i> , 2016, 33, 915-927.	8.9	119
25	Isolation and characterization of <i>Flexilinea flocculi</i> gen. nov., sp. nov., a filamentous, anaerobic bacterium belonging to the class Anaerolineae in the phylum Chloroflexi. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 988-996.	1.7	75
26	<i>Lentimicrobium saccharophilum</i> gen. nov., sp. nov., a strictly anaerobic bacterium representing a new family in the phylum Bacteroidetes, and proposal of <i>Lentimicrobiaceae</i> fam. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2635-2642.	1.7	177
27	Draft Genome Sequence of <i>Bacteroidales</i> Strain 6E, Isolated from a Rice Paddy Field in Japan. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
28	Draft Genome Sequence of <i>Bacteroidales</i> Strain TBC1, a Novel Isolate from a Methanogenic Wastewater Treatment System. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
29	Identification of Hydroxyanthraquinones as Novel Inhibitors of Hepatitis C Virus NS3 Helicase. <i>International Journal of Molecular Sciences</i> , 2015, 16, 18439-18453.	4.1	22
30	Draft Genome Sequences of <i>Anaerolinea thermolimosa</i> IMO-1, <i>Bellilinea caldifistulae</i> GOMI-1, <i>Leptolinea tardivitalis</i> YMTK-2, <i>Levilinea saccharolytica</i> KIBI-1, <i>Longilinea arvoryzae</i> KOMI-1, Previously Described as Members of the Class <i>Anaerolineae</i> (<i>Chloroflexi</i>). <i>Genome Announcements</i> , 2015, 3, .	0.8	14
31	Draft Genome Sequence of <i>Anaerolineae</i> Strain TC1, a Novel Isolate from a Methanogenic Wastewater Treatment System. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
32	A Fluorescence-Based Screening Assay for Identification of Hepatitis C Virus NS3 Helicase Inhibitors and Characterization of Their Inhibitory Mechanism. <i>Methods in Molecular Biology</i> , 2015, 1259, 211-228.	0.9	3
33	Primers: Functional Genes and 16S rRNA Genes for Methanogens. <i>Springer Protocols</i> , 2015, , 79-139.	0.3	3
34	The genome of <i>Syntrophorhabdus aromaticivorans</i> strain UI provides new insights for syntrophic aromatic compound metabolism and electron flow. <i>Environmental Microbiology</i> , 2015, 17, 4861-4872.	3.8	72
35	First genomic insights into members of a candidate bacterial phylum responsible for wastewater bulking. <i>PeerJ</i> , 2015, 3, e740.	2.0	157
36	PBDE: Structure-Activity Studies for the Inhibition of Hepatitis C Virus NS3 Helicase. <i>Molecules</i> , 2014, 19, 4006-4020.	3.8	7

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37	Identification and Biochemical Characterization of Halisulfate 3 and Suvanine as Novel Inhibitors of Hepatitis C Virus NS3 Helicase from a Marine Sponge. <i>Marine Drugs</i> , 2014, 12, 462-476.	4.6	14
38	The Phylum Gemmatimonadetes. , 2014, , 677-681.		32
39	An Expanded Genomic Representation of the Phylum Cyanobacteria. <i>Genome Biology and Evolution</i> , 2014, 6, 1031-1045.	2.5	326
40	Draft Genome Sequence of Syntrophorhabdus aromaticivorans Strain UI, a Mesophilic Aromatic Compound-Degrading Syntroph. <i>Genome Announcements</i> , 2014, 2, .	0.8	23
41	Microbial population and functional dynamics associated with surface potential and carbon metabolism. <i>ISME Journal</i> , 2014, 8, 963-978.	9.8	140
42	Lactivibrio alcoholicus gen. nov., sp. nov., an anaerobic, mesophilic, lactate-, alcohol-, carbohydrate- and amino-acid-degrading bacterium in the phylum Synergistetes. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2137-2145.	1.7	41
43	Quantitative detection of human enteric adenoviruses in river water by microfluidic digital polymerase chain reaction. <i>Water Science and Technology</i> , 2014, 70, 555-560.	2.5	16
44	Cholesterol sulfate as a potential inhibitor of hepatitis C virus NS3 helicase. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2014, 29, 223-229.	5.2	14
45	Psammaplin A inhibits hepatitis C virus NS3 helicase. <i>Journal of Natural Medicines</i> , 2013, 67, 765-772.	2.3	17
46	Oligosphaera ethanolica gen. nov., sp. nov., an anaerobic, carbohydrate-fermenting bacterium isolated from methanogenic sludge, and description of Oligosphaeria classis nov. in the phylum Lentisphaerae. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 533-539.	1.7	29
47	Inhibition of Hepatitis C Virus Replication and Viral Helicase by Ethyl Acetate Extract of the Marine Feather Star <i>Alloeocomatella polycladia</i> . <i>Marine Drugs</i> , 2012, 10, 744-761.	4.6	15
48	Quantitative detection of Cryptosporidium oocyst in water source based on 18S rRNA by alternately binding probe competitive reverse transcription polymerase chain reaction (ABC-RT-PCR). <i>Water Research</i> , 2012, 46, 187-194.	11.3	7
49	Quantitative detection of previously characterized syntrophic bacteria in anaerobic wastewater treatment systems by sequence-specific rRNA cleavage method. <i>Water Research</i> , 2012, 46, 2167-2175.	11.3	125
50	Functionally Stable and Phylogenetically Diverse Microbial Enrichments from Microbial Fuel Cells during Wastewater Treatment. <i>PLoS ONE</i> , 2012, 7, e30495.	2.5	96
51	Inhibition of Hepatitis C Virus NS3 Helicase by Manoalide. <i>Journal of Natural Products</i> , 2012, 75, 650-654.	3.0	32
52	Enhanced electrode-reducing rate during the enrichment process in an air-cathode microbial fuel cell. <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 1087-1094.	3.6	33
53	Ecological niche separation in the <i>Polynucleobacter</i> subclusters linked to quality of dissolved organic matter: a demonstration using a high sensitivity cultivation-based approach. <i>Environmental Microbiology</i> , 2012, 14, 2511-2525.	3.8	47
54	Inhibition of Both Protease and Helicase Activities of Hepatitis C Virus NS3 by an Ethyl Acetate Extract of Marine Sponge <i>Amphimedon</i> sp. <i>PLoS ONE</i> , 2012, 7, e48685.	2.5	7

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55	Oligonucleotide primers, probes and molecular methods for the environmental monitoring of methanogenic archaea. <i>Microbial Biotechnology</i> , 2011, 4, 585-602.	4.2	60
56	Alternately binding probe competitive PCR as a simple, cost-effective, and accurate quantification method for JAK2V617F allele burden in myeloproliferative neoplasms. <i>Leukemia Research</i> , 2011, 35, 1632-1636.	0.8	17
57	Ecophysiology of Uncultured Filamentous Anaerobes Belonging to the Phylum KSB3 That Cause Bulking in Methanogenic Granular Sludge. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2081-2087.	3.1	18
58	An rRNA-based analysis for evaluating the effect of heat stress on the rumen microbial composition of Holstein heifers. <i>Anaerobe</i> , 2010, 16, 27-33.	2.1	85
59	rRNA-based analysis to monitor succession of faecal bacterial communities in Holstein calves. <i>Letters in Applied Microbiology</i> , 2010, 51, 570-577.	2.2	90
60	Quantitative detection of chloroethene-reductive bacteria <i>Dehalococcoides</i> spp. using alternately binding probe competitive polymerase chain reaction. <i>Molecular and Cellular Probes</i> , 2010, 24, 131-137.	2.1	6
61	Real-time monitoring of RNA helicase activity using fluorescence resonance energy transfer in vitro. <i>Biochemical and Biophysical Research Communications</i> , 2010, 393, 131-136.	2.1	33
62	Cultivation of Methanogens under Low-Hydrogen Conditions by Using the Coculture Method. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4892-4896.	3.1	68
63	Affinity capillary electrophoresis with magnetic beads for multiplex quantitative analysis of bacterial 16S rRNA. <i>Journal of Bioscience and Bioengineering</i> , 2009, 107, 662-667.	2.2	7
64	Quantitative detection of culturable methanogenic archaea abundance in anaerobic treatment systems using the sequence-specific rRNA cleavage method. <i>ISME Journal</i> , 2009, 3, 522-535.	9.8	31
65	Effect of gelling agent on colony formation in solid cultivation of microbial community in lake sediment. <i>Environmental Microbiology</i> , 2009, 11, 1827-1834.	3.8	87
66	High-throughput screening assay of hepatitis C virus helicase inhibitors using fluorescence-quenching phenomenon. <i>Biochemical and Biophysical Research Communications</i> , 2009, 379, 1054-1059.	2.1	19
67	Universal Quenching Probe System: Flexible, Specific, and Cost-Effective Real-Time Polymerase Chain Reaction Method. <i>Analytical Chemistry</i> , 2009, 81, 5678-5685.	6.5	33
68	Comparative Analysis of Bacterial and Archaeal Communities in Methanogenic Sludge Granules from Upflow Anaerobic Sludge Blanket Reactors Treating Various Food-Processing, High-Strength Organic Wastewaters. <i>Microbes and Environments</i> , 2009, 24, 88-96.	1.6	92
69	In Situ Detection and Quantification of Uncultured Members of the Phylum Nitrospirae Abundant in Methanogenic Wastewater Treatment Systems. <i>Microbes and Environments</i> , 2009, 24, 97-104.	1.6	19
70	Cultivation of Uncultured Chloroflexi Subphyla: Significance and Ecophysiology of Formerly Uncultured Chloroflexi 'Subphylum I' with Natural and Biotechnological Relevance. <i>Microbes and Environments</i> , 2009, 24, 205-216.	1.6	247
71	Estimation of single-nucleotide polymorphism allele frequency by alternately binding probe competitive polymerase chain reaction. <i>Analytica Chimica Acta</i> , 2008, 608, 211-216.	5.4	8
72	Impact of consumption of probiotic lactobacilli-containing yogurt on microbial composition in human feces. <i>International Journal of Food Microbiology</i> , 2008, 122, 16-22.	4.7	37

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73	<i>Thermodesulfovibrio aggregans</i> sp. nov. and <i>Thermodesulfovibrio thiophilus</i> sp. nov., anaerobic, thermophilic, sulfate-reducing bacteria isolated from thermophilic methanogenic sludge, and emended description of the genus <i>Thermodesulfovibrio</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2541-2548.	1.7	121
74	<i>Methanolinea tarda</i> gen. nov., sp. nov., a methane-producing archaeon isolated from a methanogenic digester sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 294-301.	1.7	180
75	<i>Desulfovibrio marinisediminis</i> sp. nov., a novel sulfate-reducing bacterium isolated from coastal marine sediment via enrichment with Casamino acids. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2433-2438.	1.7	31
76	Comparison of Electrode Reduction Activities of <i>Geobacter sulfurreducens</i> and an Enriched Consortium in an Air-Cathode Microbial Fuel Cell. <i>Applied and Environmental Microbiology</i> , 2008, 74, 7348-7355.	3.1	192
77	<i>Syntrophorhabdus aromaticivorans</i> gen. nov., sp. nov., the First Cultured Anaerobe Capable of Degrading Phenol to Acetate in Obligate Syntrophic Associations with a Hydrogenotrophic Methanogen. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2051-2058.	3.1	219
78	<i>Desulfovibrio marinisediminis</i> sp. nov., a novel sulfate-reducing bacterium isolated from coastal marine sediment via enrichment with Casamino acids. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2673-2673.	1.7	3
79	<i>Pelotomaculum propionicicum</i> sp. nov., an anaerobic, mesophilic, obligately syntrophic, propionate-oxidizing bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 1487-1492.	1.7	94
80	<i>Anaerosporebacter mobilis</i> gen. nov., sp. nov., isolated from forest soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 1784-1787.	1.7	36
81	Methanogen Diversity in Deep Subsurface Gas-Associated Water at the Minami-Kanto Gas Field in Japan. <i>Geomicrobiology Journal</i> , 2007, 24, 93-100.	2.0	44
82	Isolation of Key Methanogens for Global Methane Emission from Rice Paddy Fields: a Novel Isolate Affiliated with the Clone Cluster Rice Cluster I. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4326-4331.	3.1	116
83	<i>Dethiosulfatibacter aminovorans</i> gen. nov., sp. nov., a novel thiosulfate-reducing bacterium isolated from coastal marine sediment via sulfate-reducing enrichment with Casamino acids. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2320-2326.	1.7	56
84	<i>Bellilinea caldifistulae</i> gen. nov., sp. nov. and <i>Longilinea arvoryzae</i> gen. nov., sp. nov., strictly anaerobic, filamentous bacteria of the phylum Chloroflexi isolated from methanogenic propionate-degrading consortia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 2299-2306.	1.7	323
85	Microbial communities in anaerobic digestion processes for waste and wastewater treatment: a microbiological update. <i>Current Opinion in Biotechnology</i> , 2007, 18, 273-278.	6.6	158
86	Characterization of filamentous bacteria, belonging to candidate phylum KSB3, that are associated with bulking in methanogenic granular sludges. <i>ISME Journal</i> , 2007, 1, 246-255.	9.8	44
87	Evaluation of group-specific, 16S rRNA-targeted scissor probes for quantitative detection of predominant bacterial populations in dairy cattle rumen. <i>Journal of Applied Microbiology</i> , 2007, 103, 1995-2005.	3.1	19
88	Phylogenetic Analysis and Fluorescence In Situ Hybridization Detection of Archaeal and Bacterial Endosymbionts in the Anaerobic Ciliate <i>Trimyema Compressum</i> . <i>Microbial Ecology</i> , 2007, 54, 627-636.	2.8	50
89	Microbial diversity and methanogenic potential in a high temperature natural gas field in Japan. <i>Extremophiles</i> , 2007, 11, 453-461.	2.3	60
90	Isolation of Uncultivated Methanogens using Anaerobic Syntrophic Substrate-degrading Coculture System.. <i>Journal of Japan Society on Water Environment</i> , 2006, 29, 389-397.	0.4	0

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91	Yet-to-be Cultured Microorganisms Relevant to Methane Fermentation Processes. <i>Microbes and Environments</i> , 2006, 21, 1-15.	1.6	55
92	Non-Sulfate-Reducing, Syntrophic Bacteria Affiliated with Desulfotomaculum Cluster I Are Widely Distributed in Methanogenic Environments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2080-2091.	3.1	165
93	<i>Pelotomaculum terephthalicum</i> sp. nov. and <i>Pelotomaculum isophthalicum</i> sp. nov.: two anaerobic bacteria that degrade phthalate isomers in syntrophic association with hydrogenotrophic methanogens. <i>Archives of Microbiology</i> , 2006, 185, 172-182.	2.2	109
94	Application of Pseudomurein Endoisopeptidase to Fluorescence In Situ Hybridization of Methanogens within the Family Methanobacteriaceae. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6907-6913.	3.1	43
95	<i>Tepidanaerobacter syntrophicus</i> gen. nov., sp. nov., an anaerobic, moderately thermophilic, syntrophic alcohol- and lactate-degrading bacterium isolated from thermophilic digested sludges. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 1621-1629.	1.7	82
96	<i>Anaerolinea thermolimos</i> sp. nov., <i>Levilinea saccharolytica</i> gen. nov., sp. nov. and <i>Leptolinea tardivitalis</i> gen. nov., sp. nov., novel filamentous anaerobes, and description of the new classes <i>Anaerolineae</i> classis nov. and <i>Caldilineae</i> classis nov. in the bacterial phylum Chloroflexi. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 1331-1340.	1.7	584
97	Filamentous Microorganisms Affiliated with Uncultured Bacterial Group at Phylum Level: Microbes as Causative Agent for Filamentous Bulking of Methanogenic Sludge Granules. <i>Journal of Japan Society on Water Environment</i> , 2005, 28, 37-42.	0.4	0
98	Comparative Analysis of Bacterial Diversity in Freshwater Sediment of a Shallow Eutrophic Lake by Molecular and Improved Cultivation-Based Techniques. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2162-2169.	3.1	240
99	Diversity, Localization, and Physiological Properties of Filamentous Microbes Belonging to Chloroflexi Subphylum I in Mesophilic and Thermophilic Methanogenic Sludge Granules. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7493-7503.	3.1	236
100	<i>Clostridium jejuense</i> sp. nov., isolated from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 1465-1468.	1.7	27
101	Identification and Isolation of Anaerobic, Syntrophic Phthalate Isomer-Degrading Microbes from Methanogenic Sludges Treating Wastewater from Terephthalate Manufacturing. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1617-1626.	3.1	80
102	Sequence-Specific Cleavage of Small-Subunit (SSU) rRNA with Oligonucleotides and RNase H: a Rapid and Simple Approach to SSU rRNA-Based Quantitative Detection of Microorganisms. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3650-3663.	3.1	39
103	Archaeal community compositions at different depths (up to 30 m) of a municipal solid waste landfill in Taiwan as revealed by 16S rDNA cloning analyses. <i>Biotechnology Letters</i> , 2003, 25, 719-724.	2.2	36
104	Molecular detection and direct enumeration of methanogenic Archaea and methanotrophic Bacteria in domestic solid waste landfill soils. <i>Biotechnology Letters</i> , 2003, 25, 1563-1569.	2.2	37
105	<i>Gemmatimonas aurantiaca</i> gen. nov., sp. nov., a Gram-negative, aerobic, polyphosphate-accumulating micro-organism, the first cultured representative of the new bacterial phylum <i>Gemmatimonadetes</i> phyl. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1155-1163.	1.7	458
106	<i>Sporotomaculum syntrophicum</i> sp. nov., a novel anaerobic, syntrophic benzoate-degrading bacterium isolated from methanogenic sludge treating wastewater from terephthalate manufacturing. <i>Archives of Microbiology</i> , 2003, 179, 242-249.	2.2	48
107	<i>Anaerolinea thermophila</i> gen. nov., sp. nov. and <i>Caldilinea aerophila</i> gen. nov., sp. nov., novel filamentous thermophiles that represent a previously uncultured lineage of the domain Bacteria at the subphylum level. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 1843-1851.	1.7	306
108	<i>Pelotomaculum thermopropionicum</i> gen. nov., sp. nov., an anaerobic, thermophilic, syntrophic propionate-oxidizing bacterium. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 1729-1735.	1.7	167

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109	å«Eæ°—æ€\$â¼ç”ÿç%©ã®ä»£è-ç%¹æ€\$:ãf jã,çãf³ç”ÿæ^âç°èEã,’ä,âçfã”ã—ã†. Nippon Nogeikagaku Kaishi, 2002, 76, 701-723.		
110	<i>Pelotomaculum thermopropionicum</i> gen. nov., sp. nov., an anaerobic, thermophilic, syntrophic propionate-oxidizing bacterium.. International Journal of Systematic and Evolutionary Microbiology, 2002, 52, 1729-1735.	1.7	140
111	Recent advances in methane fermentation technology. Current Opinion in Biotechnology, 2001, 12, 277-282.	6.6	72
112	In Situ Detection, Isolation, and Physiological Properties of a Thin Filamentous Microorganism Abundant in Methanogenic Granular Sludges: a Novel Isolate Affiliated with a Clone Cluster, the Green Non-Sulfur Bacteria, Subdivision I. Applied and Environmental Microbiology, 2001, 67, 5740-5749.	3.1	120
113	Cultivation and In Situ Detection of a Thermophilic Bacterium Capable of Oxidizing Propionate in Syntrophic Association with Hydrogenotrophic Methanogens in a Thermophilic Methanogenic Granular Sludge. Applied and Environmental Microbiology, 2000, 66, 3608-3615.	3.1	112
114	<i>Syntrophothermus lipocalidus</i> gen. nov., sp. nov., a novel thermophilic, syntrophic, fatty-acid-oxidizing anaerobe which utilizes isobutyrate.. International Journal of Systematic and Evolutionary Microbiology, 2000, 50, 771-779.	1.7	194
115	Fluorescence In Situ Hybridization Using 16S rRNA-Targeted Oligonucleotides Reveals Localization of Methanogens and Selected Uncultured Bacteria in Mesophilic and Thermophilic Sludge Granules. Applied and Environmental Microbiology, 1999, 65, 1280-1288.	3.1	394
116	Phylogenetic diversity of mesophilic and thermophilic granular sludges determined by 16S rRNA gene analysis. Microbiology (United Kingdom), 1998, 144, 2655-2665.	1.8	309
117	A novel and cost-effective sewage treatment system consisting of UASB pre-treatment and aerobic post-treatment units for developing countries. Water Science and Technology, 1997, 36, 189.	2.5	79