

Fumito Maruyama

List of Publications by Year in descending order

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Version: 2024-02-01

110
papers

4,639
citations

117453

34
h-index

114278

63
g-index

121
all docs

121
docs citations

121
times ranked

6900
citing authors

#	ARTICLE	IF	CITATIONS
1	The effect of iron on Chilean <i>Alexandrium catenella</i> growth and paralytic shellfish toxin production as related to algal blooms. <i>BioMetals</i> , 2022, 35, 39-51.	1.8	0
2	Characteristics of PM2.5 Pollution in Osorno, Chile: Ion Chromatography and Meteorological Data Analyses. <i>Atmosphere</i> , 2022, 13, 168.	1.0	2
3	Fabrication of a new all-in-one microfluidic dielectrophoresis integrated chip and living cell separation. <i>IScience</i> , 2022, 25, 103776.	1.9	10
4	Direct Attachment with Erythrocytes Augments Extracellular Growth of Pathogenic Mycobacteria. <i>Microbiology Spectrum</i> , 2022, , e0245421.	1.2	0
5	Suitcase Lab: new, portable, and deployable equipment for rapid detection of specific harmful algae in Chilean coastal waters. <i>Environmental Science and Pollution Research</i> , 2021, 28, 14144-14155.	2.7	8
6	<i>Vibrio</i> sp. ArtGut-C1, a polyhydroxybutyrate producer isolated from the gut of the aquaculture live diet <i>Artemia</i> (Crustacea). <i>Electronic Journal of Biotechnology</i> , 2021, 49, 22-28.	1.2	3
7	Capsular polysaccharide switching in <i>Streptococcus suis</i> modulates host cell interactions and virulence. <i>Scientific Reports</i> , 2021, 11, 6513.	1.6	18
8	16S rRNA-Based Analysis Reveals Differences in the Bacterial Community Present in Tissues of <i>Choromytilus chorus</i> (Mytilidae, Bivalvia) Grown in an Estuary and a Bay in Southern Chile. <i>Diversity</i> , 2021, 13, 209.	0.7	2
9	CRISPR loci-PCR as Tool for Tracking <i>Azospirillum</i> sp. Strain B510. <i>Microorganisms</i> , 2021, 9, 1351.	1.6	2
10	A Standardized Procedure for Monitoring Harmful Algal Blooms in Chile by Metabarcoding Analysis. <i>Journal of Visualized Experiments</i> , 2021, , .	0.2	1
11	Relationship between the Microbiome and Indoor Temperature/Humidity in a Traditional Japanese House with a Thatched Roof in Kyoto, Japan. <i>Diversity</i> , 2021, 13, 475.	0.7	9
12	Impact of Hinoki Cypress Wood on Diversity of Microflora: A Case Study from Owase City Hall. <i>Diversity</i> , 2021, 13, 473.	0.7	2
13	Persistent colonization of non-lymphoid tissue-resident macrophages by <i>Stenotrophomonas maltophilia</i> . <i>International Immunology</i> , 2020, 32, 133-141.	1.8	6
14	Airborne bacterial communities of outdoor environments and their associated influencing factors. <i>Environment International</i> , 2020, 145, 106156.	4.8	97
15	Isolation and Characterization of Cold-Tolerant Hyper-ACC-Degrading Bacteria from the Rhizosphere, Endosphere, and Phyllosphere of Antarctic Vascular Plants. <i>Microorganisms</i> , 2020, 8, 1788.	1.6	16
16	Size resolved characteristics of urban and suburban bacterial bioaerosols in Japan as assessed by 16S rRNA amplicon sequencing. <i>Scientific Reports</i> , 2020, 10, 12406.	1.6	17
17	Evaluation of PCR conditions for characterizing bacterial communities with full-length 16S rRNA genes using a portable nanopore sequencer. <i>Scientific Reports</i> , 2020, 10, 12580.	1.6	27
18	Continuation and replacement of <i>Vibrio cholerae</i> non-O1 clonal genomic groups isolated from <i>Plecoglossus altivelis</i> fish in freshwaters. <i>Environmental Microbiology</i> , 2020, 22, 4473-4484.	1.8	3

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19	Protocols for Monitoring Harmful Algal Blooms for Sustainable Aquaculture and Coastal Fisheries in Chile. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 7642.	1.2	17
20	Isolation and Characterization of Antimicrobial-Resistant <i>Escherichia coli</i> from Retail Meats from Roadside Butcheries in Uganda. <i>Foodborne Pathogens and Disease</i> , 2020, 17, 666-671.	0.8	1
21	Ecogenomics of the Marine Benthic Filamentous Cyanobacterium <i>Adonisia</i> . <i>Microbial Ecology</i> , 2020, 80, 249-265.	1.4	4
22	Emergence of a Multidrug-Resistant <i>Enterobacter hormaechei</i> Clinical Isolate from Egypt Co-Harboring <i>mcr-9</i> and <i>blaVIM-4</i> . <i>Microorganisms</i> , 2020, 8, 595.	1.6	32
23	Complete Genome Sequence of <i>Helicobacter pylori</i> Strain ATCC 43504, a Type Strain That Can Infect Gerbils. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	9
24	Editorial: Bioprospecting and Biotechnology of Extremophiles. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 204.	2.0	27
25	Genomewide Assessment of <i>Mycobacterium tuberculosis</i> Conditionally Essential Metabolic Pathways. <i>MSystems</i> , 2019, 4, .	1.7	59
26	The recombination-cold region as an epidemiological marker of recombinogenic opportunistic pathogen <i>Mycobacterium avium</i> . <i>BMC Genomics</i> , 2019, 20, 752.	1.2	7
27	Genetic relatedness of <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> isolates from bathrooms of healthy volunteers, rivers, and soils in Japan with human clinical isolates from different geographical areas. <i>Infection, Genetics and Evolution</i> , 2019, 74, 103923.	1.0	15
28	Draft genome sequences of <i>Mycobacterium peregrinum</i> isolated from a pig with lymphadenitis and from soil on the same Japanese pig farm. <i>BMC Research Notes</i> , 2019, 12, 341.	0.6	4
29	Application of serial tests for <i>Mycobacterium tuberculosis</i> detection to active lung tuberculosis cases in Indonesia. <i>BMC Research Notes</i> , 2019, 12, 313.	0.6	6
30	Antarctic <i>Streptomyces fildesensis</i> So13.3 strain as a promising source for antimicrobials discovery. <i>Scientific Reports</i> , 2019, 9, 7488.	1.6	27
31	Airborne Microbial Communities at High-Altitude and Suburban Sites in Toyama, Japan Suggest a New Perspective for Bioprospecting. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 12.	2.0	24
32	Genotypic diversity of <i>Streptococcus suis</i> and the <i>S. suis</i> -like bacterium <i>Streptococcus ruminantium</i> in ruminants. <i>Veterinary Research</i> , 2019, 50, 94.	1.1	13
33	Current opinion and perspectives on the methods for tracking and monitoring plant growth-promoting bacteria. <i>Soil Biology and Biochemistry</i> , 2019, 130, 205-219.	4.2	102
34	Phenotypic and genotypic analyses of antimicrobial resistant bacteria in livestock in Uganda. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 317-326.	1.3	28
35	Draft genome sequences of bacteria isolated from the <i>Deschampsia antarctica</i> phyllosphere. <i>Extremophiles</i> , 2018, 22, 537-552.	0.9	19
36	Complete Genome Sequence of the Nonheterocystous Cyanobacterium <i>Pseudanabaena</i> sp. ABRG5-3. <i>Genome Announcements</i> , 2018, 6, .	0.8	4

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37	<i>Vibrio cholerae</i> embraces two major evolutionary traits as revealed by targeted gene sequencing. <i>Scientific Reports</i> , 2018, 8, 1631.	1.6	2
38	Draft Genome Sequences of <i>Mycolicibacter senuensis</i> Isolate GF74 and <i>Mycobacterium colombiense</i> Isolates GF28 and GF76 from a Swine Farm in Japan. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	16
39	Draft Genome Sequence of a <i>Shewanella halifaxensis</i> Strain Isolated from the Intestine of Marine Red Seabream (<i>Pagrus major</i>), Which Includes an Integrative Conjugative Element with Macrolide Resistance Genes. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
40	Interplay of a non-conjugative integrative element and a conjugative plasmid in the spread of antibiotic resistance via suicidal plasmid transfer from an aquaculture <i>Vibrio</i> isolate. <i>PLoS ONE</i> , 2018, 13, e0198613.	1.1	10
41	Loss of Bacitracin Resistance Due to a Large Genomic Deletion among <i>Bacillus anthracis</i> Strains. <i>MSystems</i> , 2018, 3, .	1.7	9
42	Assessment of pig saliva as a <i>Streptococcus suis</i> reservoir and potential source of infection on farms by use of a novel quantitative polymerase chain reaction assay. <i>American Journal of Veterinary Research</i> , 2018, 79, 941-948.	0.3	14
43	Draft Genome Sequence of <i>Mycobacterium virginiense</i> Strain GF75, Isolated from the Mud of a Swine Farm in Japan. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
44	A Locus Encoding Variable Defense Systems against Invading DNA Identified in <i>Streptococcus suis</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 1000-1012.	1.1	17
45	Genetic diversity of environmental <i>Vibrio cholerae</i> O1 strains isolated in Northern Vietnam. <i>Infection, Genetics and Evolution</i> , 2017, 54, 146-151.	1.0	7
46	Population Structure and Local Adaptation of MAC Lung Disease Agent <i>Mycobacterium avium</i> subsp. <i>hominissuis</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 2403-2417.	1.1	75
47	Infection Sources of a Common Non-tuberculous Mycobacterial Pathogen, <i>Mycobacterium avium</i> Complex. <i>Frontiers in Medicine</i> , 2017, 4, 27.	1.2	153
48	Genomic Characteristics of <i>Bifidobacterium thermacidophilum</i> Pig Isolates and Wild Boar Isolates Reveal the Unique Presence of a Putative Mobile Genetic Element with <i>tetW</i> for Pig Farm Isolates. <i>Frontiers in Microbiology</i> , 2017, 8, 1540.	1.5	14
49	Transmission of Airborne Bacteria across Built Environments and Its Measurement Standards: A Review. <i>Frontiers in Microbiology</i> , 2017, 8, 2336.	1.5	86
50	YvqE and CovRS of Group A <i>Streptococcus</i> Play a Pivotal Role in Viability and Phenotypic Adaptations to Multiple Environmental Stresses. <i>PLoS ONE</i> , 2017, 12, e0170612.	1.1	11
51	Investigation of potential targets of <i>Porphyromonas</i> CRISPRs among the genomes of <i>Porphyromonas</i> species. <i>PLoS ONE</i> , 2017, 12, e0183752.	1.1	12
52	Enantioselective Utilization of D-Amino Acids by Deep-Sea Microorganisms. <i>Frontiers in Microbiology</i> , 2016, 7, 511.	1.5	40
53	Evolution and Phylogeny of Large DNA Viruses, Mimiviridae and Phycodnaviridae Including Newly Characterized Heterosigma akashiwo Virus. <i>Frontiers in Microbiology</i> , 2016, 7, 1942.	1.5	18
54	DNA-based culture-independent analysis detects the presence of group a streptococcus in throat samples from healthy adults in Japan. <i>BMC Microbiology</i> , 2016, 16, 237.	1.3	2

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55	Comparative Genome Analyses of <i>Streptococcus suis</i> Isolates from Endocarditis Demonstrate Persistence of Dual Phenotypic Clones. <i>PLoS ONE</i> , 2016, 11, e0159558.	1.1	6
56	Domestication and cereal feeding developed domestic pig-type intestinal microbiota in animals of <i>suidae</i> . <i>Animal Science Journal</i> , 2016, 87, 835-841.	0.6	25
57	Complete Genome Sequences of Broad-Host-Range <i>Pseudomonas aeruginosa</i> Bacteriophages ϕ R18 and ϕ S12-1. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
58	Distinct interacting core taxa in co-occurrence networks enable discrimination of polymicrobial oral diseases with similar symptoms. <i>Scientific Reports</i> , 2016, 6, 30997.	1.6	70
59	Sequencing and analysis of the complete organellar genomes of <i>Parmales</i> , a closely related group to <i>Bacillariophyta</i> (diatoms). <i>Current Genetics</i> , 2016, 62, 887-896.	0.8	31
60	Effect of phosphorus addition on total and alkaline phosphomonoesterase-harboring bacterial populations in ryegrass rhizosphere microsites. <i>Biology and Fertility of Soils</i> , 2016, 52, 1007-1019.	2.3	83
61	Rhizobacterial Community Structures Associated with Native Plants Grown in Chilean Extreme Environments. <i>Microbial Ecology</i> , 2016, 72, 633-646.	1.4	53
62	Deep sequencing analysis of the heterogeneity of seed and commercial lots of the <i>Bacillus Calmette-Guérin</i> (BCG) tuberculosis vaccine substrain Tokyo-172. <i>Scientific Reports</i> , 2015, 5, 17827.	1.6	10
63	Identification of a gene cluster responsible for hydrogen evolution in <i>Vibrio tritonius</i> strain AM2 with transcriptional analyses. <i>International Journal of Hydrogen Energy</i> , 2015, 40, 9137-9146.	3.8	7
64	Time-series metagenomic analysis reveals robustness of soil microbiome against chemical disturbance. <i>DNA Research</i> , 2015, 22, 413-424.	1.5	39
65	Genetic profiles of <i>Propionibacterium acnes</i> and identification of a unique transposon with novel insertion sequences in sarcoid and non-sarcoid isolates. <i>Scientific Reports</i> , 2015, 5, 9832.	1.6	12
66	Comparative genome analysis and identification of competitive and cooperative interactions in a polymicrobial disease. <i>ISME Journal</i> , 2015, 9, 629-642.	4.4	32
67	Novel macrolide-resistance genes, <i>mef</i> (C) and <i>mph</i> (G), carried by plasmids from <i>Vibrio</i> and <i>Photobacterium</i> isolated from sediment and seawater of a coastal aquaculture site. <i>Letters in Applied Microbiology</i> , 2015, 61, 1-6.	1.0	43
68	Characterization of 3 Megabase-Sized Circular Replicons from <i>Vibrio cholerae</i> . <i>Emerging Infectious Diseases</i> , 2015, 21, 1262-1263.	2.0	6
69	Reappraisal of the taxonomy of <i>Streptococcus suis</i> serotypes 20, 22 and 26: <i>Streptococcus parasuis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 438-443.	0.8	66
70	Comparative Genomic Characterization of a Thailand-Myanmar Isolate, MS6, of <i>Vibrio cholerae</i> O1 El Tor, Which Is Phylogenetically Related to a US Gulf Coast Clone. <i>PLoS ONE</i> , 2014, 9, e98120.	1.1	15
71	Various pAQU plasmids possibly contribute to disseminate tetracycline resistance gene <i>tet</i> (M) among marine bacterial community. <i>Frontiers in Microbiology</i> , 2014, 5, 152.	1.5	36
72	Genome Sequence of a <i>Bacillus anthracis</i> Outbreak Strain from Zambia, 2011. <i>Genome Announcements</i> , 2014, 2, .	0.8	13

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73	Analysis of the factors affecting the formation of the microbiome associated with chronic osteomyelitis of the jaw. <i>Clinical Microbiology and Infection</i> , 2014, 20, O309-O317.	2.8	21
74	Rab17-mediated recycling endosomes contribute to autophagosome formation in response to Group A <i>Streptococcus</i> invasion. <i>Cellular Microbiology</i> , 2014, 16, 1806-1821.	1.1	37
75	Analysis of the complete plastid genome of the unicellular red alga <i>Porphyridium purpureum</i> . <i>Journal of Plant Research</i> , 2014, 127, 389-397.	1.2	45
76	<i>Klebsormidium flaccidum</i> genome reveals primary factors for plant terrestrial adaptation. <i>Nature Communications</i> , 2014, 5, 3978.	5.8	532
77	Development of a Two-Step Multiplex PCR Assay for Typing of Capsular Polysaccharide Synthesis Gene Clusters of <i>Streptococcus suis</i> . <i>Journal of Clinical Microbiology</i> , 2014, 52, 1714-1719.	1.8	74
78	Bacterial community structures in rhizosphere microsites of ryegrass (<i>Lolium perenne</i> var. Nui) as revealed by pyrosequencing. <i>Biology and Fertility of Soils</i> , 2014, 50, 1253-1266.	2.3	31
79	The nitrogen cycle in cryoconites: naturally occurring nitrification–denitrification granules on a glacier. <i>Environmental Microbiology</i> , 2014, 16, 3250-3262.	1.8	72
80	Design and Experimental Application of a Novel Non-Degenerate Universal Primer Set that Amplifies Prokaryotic 16S rRNA Genes with a Low Possibility to Amplify Eukaryotic rRNA Genes. <i>DNA Research</i> , 2014, 21, 217-227.	1.5	432
81	Intraindividual variation in core microbiota in peri-implantitis and periodontitis. <i>Scientific Reports</i> , 2014, 4, 6602.	1.6	139
82	Phytate addition to soil induces changes in the abundance and expression of <i>Bacillus</i> –propeller phytase genes in the rhizosphere. <i>FEMS Microbiology Ecology</i> , 2013, 83, 352-360.	1.3	29
83	Whole-Genome Sequence of the Purple Photosynthetic Bacterium <i>Rhodovulum sulfidophilum</i> Strain W4. <i>Genome Announcements</i> , 2013, 1, .	0.8	16
84	CRISPR Regulation of Intraspecies Diversification by Limiting IS Transposition and Intercellular Recombination. <i>Genome Biology and Evolution</i> , 2013, 5, 1099-1114.	1.1	38
85	Genetic Analysis of Capsular Polysaccharide Synthesis Gene Clusters from All Serotypes of <i>Streptococcus suis</i> : Potential Mechanisms for Generation of Capsular Variation. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2796-2806.	1.4	88
86	Complete Genome Sequence of a <i>Propionibacterium acnes</i> Isolate from a Sarcoidosis Patient. <i>Genome Announcements</i> , 2013, 1, .	0.8	14
87	Updating the <i>Vibrio</i> clades defined by multilocus sequence phylogeny: proposal of eight new clades, and the description of <i>Vibrio tritonius</i> sp. nov.. <i>Frontiers in Microbiology</i> , 2013, 4, 414.	1.5	264
88	Complete Genome Sequence of <i>Acidovorax</i> sp. Strain KKS102, a Polychlorinated-Biphenyl Degradator. <i>Journal of Bacteriology</i> , 2012, 194, 6970-6971.	1.0	117
89	Complete Genome Sequence of the Serotype k <i>Streptococcus mutans</i> Strain LJ23. <i>Journal of Bacteriology</i> , 2012, 194, 2754-2755.	1.0	20
90	Novel Conjugative Transferable Multiple Drug Resistance Plasmid pAQU1 from <i>Photobacterium damsela</i> subsp. <i>damsela</i> ; Isolated from Marine Aquaculture Environment. <i>Microbes and Environments</i> , 2012, 27, 263-272.	0.7	87

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91	The small GTPases Rab9A and Rab23 function at distinct steps in autophagy during Group A Streptococcus infection. <i>Cellular Microbiology</i> , 2012, 14, 1149-1165.	1.1	77
92	Transition metal ions induce carnosinase activity in PepD-homologous protein from <i>Porphyromonas gingivalis</i> . <i>Microbial Pathogenesis</i> , 2012, 52, 17-24.	1.3	7
93	Genomic Structure of the Cyanobacterium <i>Synechocystis</i> sp. PCC 6803 Strain GT-S. <i>DNA Research</i> , 2011, 18, 393-399.	1.5	42
94	Complete Genome Sequence of the Bacterium <i>Porphyromonas gingivalis</i> TDC60, Which Causes Periodontal Disease. <i>Journal of Bacteriology</i> , 2011, 193, 4259-4260.	1.0	54
95	CRISPR Inhibition of Prophage Acquisition in <i>Streptococcus pyogenes</i> . <i>PLoS ONE</i> , 2011, 6, e19543.	1.1	102
96	VITCOMIC: visualization tool for taxonomic compositions of microbial communities based on 16S rRNA gene sequences. <i>BMC Bioinformatics</i> , 2010, 11, 332.	1.2	25
97	Reactive oxygen species induced by <i>Streptococcus pyogenes</i> invasion trigger apoptotic cell death in infected epithelial cells. <i>Cellular Microbiology</i> , 2010, 12, 814-830.	1.1	26
98	The Dawning Era of Comprehensive Transcriptome Analysis in Cellular Microbiology. <i>Frontiers in Microbiology</i> , 2010, 1, 118.	1.5	4
99	Specific Behavior of Intracellular <i>Streptococcus pyogenes</i> That Has Undergone Autophagic Degradation Is Associated with Bacterial Streptolysin O and Host Small G Proteins Rab5 and Rab7. <i>Journal of Biological Chemistry</i> , 2010, 285, 22666-22675.	1.6	71
100	Comparative genomic analyses of <i>Streptococcus mutans</i> provide insights into chromosomal shuffling and species-specific content. <i>BMC Genomics</i> , 2009, 10, 358.	1.2	72
101	Cost effective DNA sequencing and template preparation from bacterial colonies and plasmids. <i>Journal of Bioscience and Bioengineering</i> , 2009, 107, 471-473.	1.1	3
102	<i>Streptococcus pyogenes</i> degrades extracellular matrix in chondrocytes via MMP-13. <i>Biochemical and Biophysical Research Communications</i> , 2008, 373, 450-454.	1.0	10
103	Application of Real-Time Long and Short Polymerase Chain Reaction for Sensitive Monitoring of the Fate of Extracellular Plasmid DNA Introduced into River Waters. <i>Microbes and Environments</i> , 2008, 23, 229-236.	0.7	4
104	Current and Future Biotechnological Applications of Bacterial Phytases and Phytase-Producing Bacteria. <i>Microbes and Environments</i> , 2008, 23, 182-191.	0.7	149
105	Molecular Evidence for the Ancient Origin of the Ribosomal Protection Protein That Mediates Tetracycline Resistance in Bacteria. <i>Journal of Molecular Evolution</i> , 2007, 65, 228-235.	0.8	39
106	Quantitative Determination of Free-DNA Uptake in River Bacteria at the Single-Cell Level by In Situ Rolling-Circle Amplification. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6248-6256.	1.4	18
107	Visualization and Enumeration of Bacteria Carrying a Specific Gene Sequence by In Situ Rolling Circle Amplification. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7933-7940.	1.4	32
108	Simplified sample preparation using frame spotting method for direct counting of total bacteria by fluorescence microscopy. <i>Journal of Microbiological Methods</i> , 2004, 59, 427-431.	0.7	19

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109	Detection of Bacteria Carrying the stx2 Gene by In Situ Loop-Mediated Isothermal Amplification. Applied and Environmental Microbiology, 2003, 69, 5023-5028.	1.4	135
110	Genomic features of Mycobacterium avium subsp. hominissuis isolated from pigs in Japan. GigaByte, 0, 2021, 1-12.	0.0	3