## Yuh Shiwa

## List of Publications by Year in descending order

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54	1,072	17 h-index	30
papers	citations		g-index
56	56	56	1863 citing authors
all docs	docs citations	times ranked	

#	Article	IF	Citations
1	Draft Genome Sequence of the Polychlorinated Biphenyl Degrader Comamonas testosteroni Strain YAZ2, Isolated from a Natural Landscape in the Tohoku Region of Japan. Microbiology Resource Announcements, 2022, 11, e0080621.	0.6	1
2	Novel heat shock response mechanism mediated by the initiation nucleotide of transcription. Journal of General and Applied Microbiology, 2022, 68, 95-108.	0.7	2
3	Bacterial Community of Water Yam ( <i>Dioscorea alata</i> L.) cv. A-19. Microbes and Environments, 2022, 37, n/a.	1.6	3
4	Antagonism of Bacillus velezensis Isolate from Anaerobically Digested Dairy Slurry against Fusarium Wilt of Spinach. Agronomy, 2022, 12, 1058.	3.0	0
5	Possible clinical outcomes using early enteral nutrition in individuals with allogeneic hematopoietic stem cell transplantation: A single-center retrospective study. Nutrition, 2021, 83, 111093.	2.4	8
6	Acyl-CoA synthetases, Aal4 and Aal7, are involved in the utilization of exogenous fatty acids in <i>Yarrowia lipolytica</i> . Journal of General and Applied Microbiology, 2021, 67, 9-14.	0.7	2
7	Characterization of the microbiota and chemical properties of pork loins during dry aging. MicrobiologyOpen, 2021, 10, e1157.	3.0	6
8	Niche-specific adaptation of Lactobacillus helveticus strains isolated from malt whisky and dairy fermentations. Microbial Genomics, $2021, 7, \ldots$	2.0	5
9	Draft genome sequencing of Sporolactobacillus terrae SBT-1, an efficient bacterium to ferment concentrated sugar to d-lactic acid. Archives of Microbiology, 2021, 203, 3577-3590.	2.2	6
10	Idification and structural characterisation of a catecholate-type siderophore produced by Stenotrophomonas maltophilia K279a. Microbiology (United Kingdom), 2021, 167, .	1.8	3
11	Using pollen DNA metabarcoding to profile nectar sources of urban beekeeping in KÅŧÅ•ku, Tokyo. BMC Research Notes, 2020, 13, 515.	1.4	17
12	PCR-based screening, isolation, and partial characterization of motile lactobacilli from various animal feces. BMC Microbiology, 2020, 20, 142.	3.3	4
13	Fpr1, a primary target of rapamycin, functions as a transcription factor for ribosomal protein genesÂcooperatively with Hmo1 in Saccharomyces cerevisiae. PLoS Genetics, 2020, 16, e1008865.	3.5	14
14	Comparative Genomic Analysis of Closely Related Acetobacter pasteurianus Strains Provides Evidence of Horizontal Gene Transfer and Reveals Factors Necessary for Thermotolerance. Journal of Bacteriology, 2020, 202, .	2.2	17
15	Changed bacterial community in the river water samples upon introduction of biodegradable poly(3-hydroxybutyrate). Polymer Degradation and Stability, 2020, 176, 109144.	5.8	5
16	Rhizobium dioscoreae sp. nov., a plant growth-promoting bacterium isolated from yam (Dioscorea) Tj ETQq0 0 0	) rgBT  Ov	erlock 10 Tf 50
17	Comparative Analysis of Bacterial Diversity and Community Structure in the Rhizosphere and Root Endosphere of Two Halophytes, <i>Salicornia europaea</i> and <i>Glaux maritima</i> , Collected from Two Brackish Lakes in Japan. Microbes and Environments, 2020, 35, n/a	1.6	11
18	Transcriptome profile of carbon catabolite repression in an efficient l-(+)-lactic acid-producing bacterium Enterococcus mundtii QU25 grown in media with combinations of cellobiose, xylose, and glucose. PLoS ONE, 2020, 15, e0242070.	2.5	3

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19	The genome sequence of Streptomyces rochei 7434AN4, which carries a linear chromosome and three characteristic linear plasmids. Scientific Reports, 2019, 9, 10973.	3.3	32
20	Draft Genome Sequence of Zygosaccharomyces mellis CA-7, Isolated from Honey. Microbiology Resource Announcements, 2019, 8, .	0.6	2
21	Poly-Î <sup>3</sup> -glutamic acid production of Bacillus subtilis (natto) in the absence of DegQ: A gain-of-function mutation in yabJ gene. Journal of Bioscience and Bioengineering, 2019, 128, 690-696.	2.2	8
22	A novel intracellular dextranase derived from Paenibacillus sp. 598K with an ability to degrade cycloisomaltooligosaccharides. Applied Microbiology and Biotechnology, 2019, 103, 6581-6592.	3.6	7
23	Stable and efficient delivery of DNA toBacillus subtilis(natto) using pLS20 conjugational transfer plasmids. FEMS Microbiology Letters, 2019, 366, .	1.8	3
24	Enterococcus florum sp. nov., isolated from a cotton flower (Gossypium hirsutum L.). International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 2506-2513.	1.7	10
25	Bacterial Diversity Associated With the Rhizosphere and Endosphere of Two Halophytes: Glaux maritima and Salicornia europaea. Frontiers in Microbiology, 2018, 9, 2878.	3.5	73
26	Combined Drug Resistance Mutations Substantially Enhance Enzyme Production in Paenibacillus agaridevorans. Journal of Bacteriology, 2018, 200, .	2.2	13
27	Essentiality of WalRK for growth in Bacillus subtilis and its role during heat stress. Microbiology (United Kingdom), 2018, 164, 670-684.	1.8	14
28	Effects of <i>Lactobacillus paracasei</i> K71 on gut microbiota composition and lipid metabolism in <i>ob</i> / <i>ob</i> mice Japanese Journal of Lactic Acid Bacteria, 2018, 29, 152-157.	0.1	0
29	î"12-fatty acid desaturase is involved in growth at low temperature in yeast Yarrowia lipolytica. Biochemical and Biophysical Research Communications, 2017, 488, 165-170.	2.1	34
30	Genome Mining of Amino Group Carrier Protein-Mediated Machinery: Discovery and Biosynthetic Characterization of a Natural Product with Unique Hydrazone Unit. ACS Chemical Biology, 2017, 12, 124-131.	3.4	29
31	Comparative genomics of <i>Tetragenococcus halophilus</i> . Journal of General and Applied Microbiology, 2017, 63, 369-372.	0.7	18
32	Distribution of human singleâ€nucleotide polymorphisms is approximated by the power law and represents a fractal structure. Genes To Cells, 2016, 21, 396-407.	1.2	5
33	Eudistomin C, an Antitumor and Antiviral Natural Product, Targets 40S Ribosome and Inhibits Protein Translation. ChemBioChem, 2016, 17, 1616-1620.	2.6	13
34	Comprehensive identification of translation start sites by tetracycline-inhibited ribosome profiling. DNA Research, 2016, 23, 193-201.	3.4	83
35	Population Evolution of <i>Helicobacter pylori</i> through Diversification in DNA Methylation and Interstrain Sequence Homogenization. Molecular Biology and Evolution, 2016, 33, 2848-2859.	8.9	29
36	Growth and sporulation defects in Bacillus subtilis mutants with a single rrn operon can be suppressed by amplification of the rrn operon. Microbiology (United Kingdom), 2016, 162, 35-45.	1.8	7

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37	EliA is required for inducing the stearyl alcohol-mediated expression of secretory proteins and production of polyester in Ralstonia sp. NT80. Microbiology (United Kingdom), 2016, 162, 408-419.	1.8	0
38	Comparative genomics of Fructobacillus spp. and Leuconostoc spp. reveals niche-specific evolution of Fructobacillus spp BMC Genomics, 2015, 16, 1117.	2.8	53
39	Strigolactone Regulates Anthocyanin Accumulation, Acid Phosphatases Production and Plant Growth under Low Phosphate Condition in Arabidopsis. PLoS ONE, 2015, 10, e0119724.	2.5	50
40	Microevolution of Virulence-Related Genes in Helicobacter pylori Familial Infection. PLoS ONE, 2015, 10, e0127197.	2.5	23
41	A novel subpopulation of Salmonella enterica serovar Infantis strains isolated from broiler chicken organs other than the gastrointestinal tract. Veterinary Microbiology, 2015, 175, 312-318.	1.9	28
42	Transcriptional regulation of xylose utilization in Enterococcus mundtii QU 25. RSC Advances, 2015, 5, 93283-93292.	3.6	4
43	Plant Raf-like kinase integrates abscisic acid and hyperosmotic stress signaling upstream of SNF1-related protein kinase2. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6388-96.	7.1	137
44	Genome Sequences of Three Strains of Lactobacillus paracasei of Different Origins and with Different Cholate Sensitivities. Genome Announcements, 2015, 3, .	0.8	3
45	Bacillus subtilis degSU operon is regulated by the ClpXP-Spx regulated proteolysis system. Journal of Biochemistry, 2015, 157, 321-330.	1.7	14
46	Genome-Wide DNA Polymorphisms in Seven Rice Cultivars of Temperate and Tropical Japonica Groups. PLoS ONE, 2014, 9, e86312.	2.5	30
47	Draft Genome Sequence of the Versatile Alkane-Degrading Bacterium <i>Aquabacterium </i> sp. Strain NJ1. Genome Announcements, 2014, 2, .	0.8	16
48	Complete Genome Sequence of Bifidobacterium longum 105-A, a Strain with High Transformation Efficiency. Genome Announcements, 2014, 2, .	0.8	16
49	Defect in the Formation of 70S Ribosomes Caused by Lack of Ribosomal Protein L34 Can Be Suppressed by Magnesium. Journal of Bacteriology, 2014, 196, 3820-3830.	2.2	64
50	Complete Genome Sequence of Enterococcus mundtii QU 25, an Efficient L-(+)-Lactic Acid-Producing Bacterium. DNA Research, 2014, 21, 369-377.	3.4	22
51	Phylogenetic and population genetic analysis of Salmonella enterica subsp. enterica serovar Infantis strains isolated in Japan using whole genome sequence data. Infection, Genetics and Evolution, 2014, 27, 62-68.	2.3	24
52	Multiple rRNA operons are essential for efficient cell growth and sporulation as well as outgrowth in Bacillus subtilis. Microbiology (United Kingdom), 2013, 159, 2225-2236.	1.8	52
53	Identification of Laboratory-Specific Variations of <i>Bacillus subtilis </i> Bioscience, Biotechnology and Biochemistry, 2013, 77, 2073-2076.	1.3	8
54	Whole-Genome Profiling of a Novel Mutagenesis Technique Using Proofreading-Deficient DNA Polymerase <mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML"><mml:mi mathvariant="bold">Î'</mml:mi></mml:math> . International Journal of Evolutionary Biology, 2012, 2012, 1-8.	1.0	25