

# Yuh Shiwa

## List of Publications by Year in descending order

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54  
papers

1,072  
citations

471509

17  
h-index

454955

30  
g-index

56  
all docs

56  
docs citations

56  
times ranked

1863  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Comprehensive identification of translation start sites by tetracycline-inhibited ribosome profiling. DNA Research, 2016, 23, 193-201.	3.4	83
3	Bacterial Diversity Associated With the Rhizosphere and Endosphere of Two Halophytes: <i>Glaux maritima</i> and <i>Salicornia europaea</i> . Frontiers in Microbiology, 2018, 9, 2878.	3.5	73
4	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
5	Comparative genomics of <i>Fructobacillus</i> spp. and <i>Leuconostoc</i> spp. reveals niche-specific evolution of <i>Fructobacillus</i> spp.. BMC Genomics, 2015, 16, 1117.	2.8	53
6	Multiple rRNA operons are essential for efficient cell growth and sporulation as well as outgrowth in <i>Bacillus subtilis</i> . Microbiology (United Kingdom), 2013, 159, 2225-2236.	1.8	52
7	Strigolactone Regulates Anthocyanin Accumulation, Acid Phosphatases Production and Plant Growth under Low Phosphate Condition in <i>Arabidopsis</i> . PLoS ONE, 2015, 10, e0119724.	2.5	50
8	Δ <sup>12</sup> -fatty acid desaturase is involved in growth at low temperature in yeast <i>Yarrowia lipolytica</i> . Biochemical and Biophysical Research Communications, 2017, 488, 165-170.	2.1	34
9	The genome sequence of <i>Streptomyces rochei</i> 7434AN4, which carries a linear chromosome and three characteristic linear plasmids. Scientific Reports, 2019, 9, 10973.	3.3	32
10	Genome-Wide DNA Polymorphisms in Seven Rice Cultivars of Temperate and Tropical Japonica Groups. PLoS ONE, 2014, 9, e86312.	2.5	30
11	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
12	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
13	A novel subpopulation of <i>Salmonella enterica</i> serovar <i>Infantis</i> strains isolated from broiler chicken organs other than the gastrointestinal tract. Veterinary Microbiology, 2015, 175, 312-318.	1.9	28
14	Whole-Genome Profiling of a Novel Mutagenesis Technique Using Proofreading-Deficient DNA Polymerase $\epsilon'$ . International Journal of Evolutionary Biology, 2012, 2012, 1-8.	1.0	25
15	Phylogenetic and population genetic analysis of <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Infantis</i> strains isolated in Japan using whole genome sequence data. Infection, Genetics and Evolution, 2014, 27, 62-68.	2.3	24
16	Microevolution of Virulence-Related Genes in <i>Helicobacter pylori</i> Familial Infection. PLoS ONE, 2015, 10, e0127197.	2.5	23
17	Complete Genome Sequence of <i>Enterococcus mundtii</i> QU 25, an Efficient L-(+)-Lactic Acid-Producing Bacterium. DNA Research, 2014, 21, 369-377.	3.4	22
18	Comparative genomics of <i>Tetragenococcus halophilus</i> . Journal of General and Applied Microbiology, 2017, 63, 369-372.	0.7	18

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19	Using pollen DNA metabarcoding to profile nectar sources of urban beekeeping in K��ku, Tokyo. BMC Research Notes, 2020, 13, 515.	1.4	17
20	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
21	Draft Genome Sequence of the Versatile Alkane-Degrading Bacterium <i>Aquabacterium</i> sp. Strain NJ1. Genome Announcements, 2014, 2, .	0.8	16
22	Complete Genome Sequence of Bifidobacterium longum 105-A, a Strain with High Transformation Efficiency. Genome Announcements, 2014, 2, .	0.8	16
23	Rhizobium dioscoreae sp. nov., a plant growth-promoting bacterium isolated from yam (Dioscorea) Tj ETQq1 1 0.784314 rgBJ /Overlob	1.7	15
24	Bacillus subtilis degSU operon is regulated by the ClpXP-Spx regulated proteolysis system. Journal of Biochemistry, 2015, 157, 321-330.	1.7	14
25	Fpr1, a primary target of rapamycin, functions as a transcription factor for ribosomal protein genes cooperatively with Hmo1 in Saccharomyces cerevisiae. PLoS Genetics, 2020, 16, e1008865.	3.5	14
26	Essentiality of WalRK for growth in Bacillus subtilis and its role during heat stress. Microbiology (United Kingdom), 2018, 164, 670-684.	1.8	14
27	Eudistomin C, an Antitumor and Antiviral Natural Product, Targets 40S Ribosome and Inhibits Protein Translation. ChemBioChem, 2016, 17, 1616-1620.	2.6	13
28	Combined Drug Resistance Mutations Substantially Enhance Enzyme Production in Paenibacillus agaridevorans. Journal of Bacteriology, 2018, 200, .	2.2	13
29	Comparative Analysis of Bacterial Diversity and Community Structure in the Rhizosphere and Root Endosphere of Two Halophytes, &lt;i>Salicornia europaea&lt;/i> and &lt;i>Glaux maritima&lt;/i>, Collected from Two Brackish Lakes in Japan. Microbes and Environments, 2020, 35, n/a.	1.6	11
30	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
31	Identification of Laboratory-Specific Variations of <i>Bacillus subtilis</i> Strains Used in Japan. Bioscience, Biotechnology and Biochemistry, 2013, 77, 2073-2076.	1.3	8
32	Poly-��-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
33	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
34	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
35	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
36	Characterization of the microbiota and chemical properties of pork loins during dry aging. MicrobiologyOpen, 2021, 10, e1157.	3.0	6

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37	Draft genome sequencing of <i>Sporolactobacillus terrae</i> SBT-1, an efficient bacterium to ferment concentrated sugar to d-lactic acid. <i>Archives of Microbiology</i> , 2021, 203, 3577-3590.	2.2	6
38	Distribution of human single-nucleotide polymorphisms is approximated by the power law and represents a fractal structure. <i>Genes To Cells</i> , 2016, 21, 396-407.	1.2	5
39	Changed bacterial community in the river water samples upon introduction of biodegradable poly(3-hydroxybutyrate). <i>Polymer Degradation and Stability</i> , 2020, 176, 109144.	5.8	5
40	Niche-specific adaptation of <i>Lactobacillus helveticus</i> strains isolated from malt whisky and dairy fermentations. <i>Microbial Genomics</i> , 2021, 7, .	2.0	5
41	Transcriptional regulation of xylose utilization in <i>Enterococcus mundtii</i> QU 25. <i>RSC Advances</i> , 2015, 5, 93283-93292.	3.6	4
42	PCR-based screening, isolation, and partial characterization of motile lactobacilli from various animal feces. <i>BMC Microbiology</i> , 2020, 20, 142.	3.3	4
43	Genome Sequences of Three Strains of <i>Lactobacillus paracasei</i> of Different Origins and with Different Cholera Sensitivities. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
44	Stable and efficient delivery of DNA to <i>Bacillus subtilis</i> (natto) using pLS20 conjugational transfer plasmids. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	3
45	Identification and structural characterisation of a catecholate-type siderophore produced by <i>Stenotrophomonas maltophilia</i> K279a. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	3
46	Transcriptome profile of carbon catabolite repression in an efficient l-(+)-lactic acid-producing bacterium <i>Enterococcus mundtii</i> QU25 grown in media with combinations of cellobiose, xylose, and glucose. <i>PLoS ONE</i> , 2020, 15, e0242070.	2.5	3
47	Bacterial Community of Water Yam (&lt;i>Dioscorea alata&lt;/i> L.) cv. A-19. <i>Microbes and Environments</i> , 2022, 37, n/a.	1.6	3
48	Draft Genome Sequence of <i>Zygosaccharomyces mellis</i> CA-7, Isolated from Honey. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
49	Acyl-CoA synthetases, Aal4 and Aal7, are involved in the utilization of exogenous fatty acids in <i>Yarrowia lipolytica</i> . <i>Journal of General and Applied Microbiology</i> , 2021, 67, 9-14.	0.7	2
50	Novel heat shock response mechanism mediated by the initiation nucleotide of transcription. <i>Journal of General and Applied Microbiology</i> , 2022, 68, 95-108.	0.7	2
51	Draft Genome Sequence of the Polychlorinated Biphenyl Degradator <i>Comamonas testosteroni</i> Strain YA22, Isolated from a Natural Landscape in the Tohoku Region of Japan. <i>Microbiology Resource Announcements</i> , 2022, 11, e0080621.	0.6	1
52	EliA is required for inducing the stearyl alcohol-mediated expression of secretory proteins and production of polyester in <i>Ralstonia</i> sp. NT80. <i>Microbiology (United Kingdom)</i> , 2016, 162, 408-419.	1.8	0
53	Effects of <i>Lactobacillus paracasei</i> K71 on gut microbiota composition and lipid metabolism in mice. <i>Japanese Journal of Lactic Acid Bacteria</i> , 2018, 29, 152-157.	0.1	0
54	Antagonism of <i>Bacillus velezensis</i> Isolate from Anaerobically Digested Dairy Slurry against <i>Fusarium</i> Wilt of Spinach. <i>Agronomy</i> , 2022, 12, 1058.	3.0	0