

# Qun Wu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/840332/publications.pdf>

Version: 2024-02-01

47  
papers

2,138  
citations

201385

27  
h-index

233125

45  
g-index

48  
all docs

48  
docs citations

48  
times ranked

1139  
citing authors

#	ARTICLE	IF	CITATIONS
1	Filamentous fungal diversity and community structure associated with the solid state fermentation of Chinese Maotai-flavor liquor. <i>International Journal of Food Microbiology</i> , 2014, 179, 80-84.	2.1	149
2	<i>Bacillus licheniformis</i> affects the microbial community and metabolic profile in the spontaneous fermentation of Daqu starter for Chinese liquor making. <i>International Journal of Food Microbiology</i> , 2017, 250, 59-67.	2.1	145
3	Yeast community associated with the solid state fermentation of traditional Chinese Maotai-flavor liquor. <i>International Journal of Food Microbiology</i> , 2013, 166, 323-330.	2.1	130
4	Systematically engineering the biosynthesis of a green biosurfactant surfactin by <i>Bacillus subtilis</i> 168. <i>Metabolic Engineering</i> , 2019, 52, 87-97.	3.6	118
5	Can we control microbiota in spontaneous food fermentation? â€“ Chinese liquor as a case example. <i>Trends in Food Science and Technology</i> , 2021, 110, 321-331.	7.8	112
6	Construction of Synthetic Microbiota for Reproducible Flavor Compound Metabolism in Chinese Light-Aroma-Type Liquor Produced by Solid-State Fermentation. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	107
7	Genome and transcriptome analysis of surfactin biosynthesis in <i>Bacillus amyloliquefaciens</i> MT45. <i>Scientific Reports</i> , 2017, 7, 40976.	1.6	84
8	<i>In Situ</i> Analysis of Metabolic Characteristics Reveals the Key Yeast in the Spontaneous and Solid-State Fermentation Process of Chinese Light-Style Liquor. <i>Applied and Environmental Microbiology</i> , 2014, 80, 3667-3676.	1.4	80
9	Production of surfactin from waste distillersâ€™ grains by co-culture fermentation of two <i>Bacillus amyloliquefaciens</i> strains. <i>Bioresource Technology</i> , 2017, 235, 96-103.	4.8	80
10	Improving flavor metabolism of <i>Saccharomyces cerevisiae</i> by mixed culture with <i>Bacillus licheniformis</i> for Chinese Maotai-flavor liquor making. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015, 42, 1601-1608.	1.4	76
11	Synergistic Effect of Multiple Saccharifying Enzymes on Alcoholic Fermentation for Chinese Baijiu Production. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	64
12	Starter Culture Selection for Making Chinese Sesame-Flavored Liquor Based on Microbial Metabolic Activity in Mixed-Culture Fermentation. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4450-4459.	1.4	59
13	Synergistic Effect in Core Microbiota Associated with Sulfur Metabolism in Spontaneous Chinese Liquor Fermentation. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	54
14	Effect of yeast species on the terpenoids profile of Chinese light-style liquor. <i>Food Chemistry</i> , 2015, 168, 390-395.	4.2	49
15	Flavor Profile of Chinese Liquor Is Altered by Interactions of Intrinsic and Extrinsic Microbes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 422-430.	1.4	47
16	Temperature-Induced Annual Variation in Microbial Community Changes and Resulting Metabolome Shifts in a Controlled Fermentation System. <i>MSystems</i> , 2020, 5, .	1.7	47
17	<i>Zygosaccharomyces bailii</i> Is a Potential Producer of Various Flavor Compounds in Chinese Maotai-Flavor Liquor Fermentation. <i>Frontiers in Microbiology</i> , 2017, 8, 2609.	1.5	46
18	Modeling and Regulation of Higher Alcohol Production through the Combined Effects of the C/N Ratio and Microbial Interaction. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 10694-10701.	2.4	45

#	ARTICLE	IF	CITATIONS
19	Biocontrol of geosmin-producing <i>Streptomyces</i> spp. by two <i>Bacillus</i> strains from Chinese liquor. <i>International Journal of Food Microbiology</i> , 2016, 231, 1-9.	2.1	41
20	Chinese Liquor Fermentation: Identification of Key Flavor-Producing <i>Lactobacillus</i> spp. by Quantitative Profiling with Indigenous Internal Standards. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	41
21	Raw Material Regulates Flavor Formation via Driving Microbiota in Chinese Liquor Fermentation. <i>Frontiers in Microbiology</i> , 2019, 10, 1520.	1.5	40
22	Biodegradation of Ethyl Carbamate and Urea with <i>Lysinibacillus sphaericus</i> MT33 in Chinese Liquor Fermentation. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 1583-1590.	2.4	39
23	Specific Volumetric Weight-Driven Shift in Microbiota Compositions With Saccharifying Activity Change in Starter for Chinese Baijiu Fermentation. <i>Frontiers in Microbiology</i> , 2018, 9, 2349.	1.5	39
24	<i>Zygosaccharomyces pseudobailii</i> , another yeast interspecies hybrid that regained fertility by damaging one of its MAT loci. <i>FEMS Yeast Research</i> , 2018, 18, .	1.1	39
25	Transcriptome Profiling of Heat-Resistant Strain <i>Bacillus licheniformis</i> CGMCC3962 Producing <i>Maotai</i> Flavor. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 2033-2038.	2.4	38
26	Regulating yeast flavor metabolism by controlling saccharification reaction rate in simultaneous saccharification and fermentation of Chinese Maotai-flavor liquor. <i>International Journal of Food Microbiology</i> , 2015, 200, 39-46.	2.1	36
27	Development, validation and application of specific primers for analyzing the clostridial diversity in dark fermentation pit mud by PCR-DGGE. <i>Bioresource Technology</i> , 2014, 163, 40-47.	4.8	29
28	Construction of a synthetic microbial community for the biosynthesis of volatile sulfur compound by multi-module division of labor. <i>Food Chemistry</i> , 2021, 347, 129036.	4.2	27
29	Isolation and identification of a black <i>Aspergillus</i> strain and the effect of its novel protease on the aroma of <i>Moutai</i> -flavoured liquor. <i>Journal of the Institute of Brewing</i> , 2014, 120, 268-276.	0.8	26
30	Genomic and transcriptomic analyses of the Chinese Maotai-flavored liquor yeast MT1 revealed its unique multi-carbon co-utilization. <i>BMC Genomics</i> , 2015, 16, 1064.	1.2	25
31	Immobilized <i>Rhodotorula mucilaginosa</i> : A Novel Urethanase-Producing Strain for Degrading Ethyl Carbamate. <i>Applied Biochemistry and Biotechnology</i> , 2013, 171, 2220-2232.	1.4	22
32	Sugar profile regulates the microbial metabolic diversity in Chinese Baijiu fermentation. <i>International Journal of Food Microbiology</i> , 2021, 359, 109426.	2.1	21
33	Modelling and predicting population of core fungi through processing parameters in spontaneous starter (Daqu) fermentation. <i>International Journal of Food Microbiology</i> , 2022, 363, 109493.	2.1	21
34	Fe Nanoparticles Enhanced Surfactin Production in <i>Bacillus amyloliquefaciens</i> . <i>ACS Omega</i> , 2020, 5, 6321-6329.	1.6	20
35	Increasing 2-furfurylthiol content in Chinese sesame-flavored Baijiu via inoculating the producer of precursor l-cysteine in Baijiu fermentation. <i>Food Research International</i> , 2020, 138, 109757.	2.9	19
36	Effects of glutinous and nonglutinous sorghums on <i>Saccharomyces cerevisiae</i> fermentation for Chinese liquor making. <i>International Journal of Food Science and Technology</i> , 2017, 52, 1348-1357.	1.3	17

#	ARTICLE	IF	CITATIONS
37	On-site calibration method for outdoor binocular stereo vision sensors. <i>Optics and Lasers in Engineering</i> , 2016, 86, 75-82.	2.0	15
38	Identification and quantification of surfactin, a nonvolatile lipopeptide in Moutai liquor. <i>International Journal of Food Properties</i> , 2020, 23, 189-198.	1.3	13
39	Initial fungal diversity impacts flavor compounds formation in the spontaneous fermentation of Chinese liquor. <i>Food Research International</i> , 2022, 155, 110995.	2.9	13
40	Transcriptional Characteristics Associated with Lichenysin Biosynthesis in <i>Bacillus licheniformis</i> from Chinese Maotai-Flavor Liquor Making. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 888-893.	2.4	12
41	Gradient Internal Standard Method for Absolute Quantification of Microbial Amplicon Sequencing Data. <i>MSystems</i> , 2021, 6, .	1.7	11
42	Effect of Microbial Interaction on Urea Metabolism in Chinese Liquor Fermentation. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 11133-11139.	2.4	10
43	Biodegradation of cyanide with <i>Saccharomyces cerevisiae</i> in Baijiu fermentation. <i>Food Control</i> , 2021, 127, 108107.	2.8	10
44	Urea production by yeasts other than <i>Saccharomyces</i> in food fermentation. <i>FEMS Yeast Research</i> , 2017, 17, .	1.1	7
45	Regional aroma characteristics of sorghum for Chinese liquor production. <i>Journal of the Institute of Brewing</i> , 2020, 126, 306-315.	0.8	7
46	Genome Sequence of <i>Bacillus licheniformis</i> CGMCC3963, a Stress-Resistant Strain Isolated in a Chinese Traditional Solid-State Liquor-Making Process. <i>Genome Announcements</i> , 2013, 1, .	0.8	6
47	Fast and Effective Dynamic Optimization for Chemical Processes with Catalyst Deactivation Based on Incremental Encoding and Random Search. <i>Industrial &amp; Engineering Chemistry Research</i> , 2021, 60, 2983-2993.	1.8	2