

# Bilige Menghe

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2832552/publications.pdf>

Version: 2024-02-01

28  
papers

1,405  
citations

361413

20  
h-index

454955

30  
g-index

30  
all docs

30  
docs citations

30  
times ranked

1922  
citing authors

#	ARTICLE	IF	CITATIONS
1	A phylo-functional core of gut microbiota in healthy young Chinese cohorts across lifestyles, geography and ethnicities. <i>ISME Journal</i> , 2015, 9, 1979-1990.	9.8	339
2	Isolation and preliminary probiotic selection of lactobacilli from koumiss in Inner Mongolia. <i>Journal of Basic Microbiology</i> , 2009, 49, 318-326.	3.3	119
3	Characterization of Antibiotic Resistance Genes from <i>Lactobacillus</i> Isolated from Traditional Dairy Products. <i>Journal of Food Science</i> , 2017, 82, 724-730.	3.1	111
4	Comparative Genomic Analysis of 45 Type Strains of the Genus <i>Bifidobacterium</i> : A Snapshot of Its Genetic Diversity and Evolution. <i>PLoS ONE</i> , 2015, 10, e0117912.	2.5	90
5	Effects of microencapsulated <i>Lactobacillus plantarum</i> LIP-1 on the gut microbiota of hyperlipidaemic rats. <i>British Journal of Nutrition</i> , 2017, 118, 481-492.	2.3	79
6	Characterization of potentially probiotic lactic acid bacteria and bifidobacteria isolated from human colostrum. <i>Journal of Dairy Science</i> , 2020, 103, 4013-4025.	3.4	75
7	Comparative genomic analysis of the genus <i>Enterococcus</i> . <i>Microbiological Research</i> , 2017, 196, 95-105.	5.3	53
8	Multilocus sequence typing of <i>Streptococcus thermophilus</i> from naturally fermented dairy foods in China and Mongolia. <i>BMC Microbiology</i> , 2015, 15, 236.	3.3	52
9	A Perspective Study of Koumiss Microbiome by Metagenomics Analysis Based on Single-Cell Amplification Technique. <i>Frontiers in Microbiology</i> , 2017, 8, 165.	3.5	50
10	Investigating bacterial population structure and dynamics in traditional koumiss from Inner Mongolia using single molecule real-time sequencing. <i>Journal of Dairy Science</i> , 2016, 99, 7852-7863.	3.4	40
11	Carbohydrate Staple Food Modulates Gut Microbiota of Mongolians in China. <i>Frontiers in Microbiology</i> , 2017, 8, 484.	3.5	40
12	Identification and characterization of the dominant lactobacilli isolated from koumiss in China. <i>Journal of General and Applied Microbiology</i> , 2010, 56, 257-265.	0.7	39
13	Short communication: Single molecule, real-time sequencing technology revealed species- and strain-specific methylation patterns of 2 <i>Lactobacillus</i> strains. <i>Journal of Dairy Science</i> , 2015, 98, 3020-3024.	3.4	38
14	Profiling of koumiss microbiota and organic acids and their effects on koumiss taste. <i>BMC Microbiology</i> , 2020, 20, 85.	3.3	37
15	Isolation and Identification of Lactic Acid Bacteria from Traditional Dairy Products in Baotou and Bayannur of Midwestern Inner Mongolia and q-PCR Analysis of Predominant Species. <i>Korean Journal for Food Science of Animal Resources</i> , 2016, 36, 499-507.	1.5	30
16	Relationships between functional genes in <i>Lactobacillus delbrueckii</i> ssp. <i>bulgaricus</i> isolates and phenotypic characteristics associated with fermentation time and flavor production in yogurt elucidated using multilocus sequence typing. <i>Journal of Dairy Science</i> , 2016, 99, 89-103.	3.4	28
17	The evolution and population structure of <i>Lactobacillus fermentum</i> from different naturally fermented products as determined by multilocus sequence typing (MLST). <i>BMC Microbiology</i> , 2015, 15, 107.	3.3	27
18	Multilocus sequence typing of <i>Lactobacillus casei</i> isolates from naturally fermented foods in China and Mongolia. <i>Journal of Dairy Science</i> , 2016, 99, 5202-5213.	3.4	27

#	ARTICLE	IF	CITATIONS
19	Multilocus sequence typing of <i>Lactococcus lactis</i> from naturally fermented milk foods in ethnic minority areas of China. <i>Journal of Dairy Science</i> , 2014, 97, 2633-2645.	3.4	24
20	A Metabolomics Approach Uncovers Differences between Traditional and Commercial Dairy Products in Buryatia (Russian Federation). <i>Molecules</i> , 2018, 23, 735.	3.8	24
21	Genetic diversity and population structure of <i>Lactobacillus delbrueckii</i> subspecies <i>bulgaricus</i> isolated from naturally fermented dairy foods. <i>Scientific Reports</i> , 2016, 6, 22704.	3.3	16
22	Comparison of Bacterial Microbiota in Raw Mare's Milk and Koumiss Using PacBio Single Molecule Real-Time Sequencing Technology. <i>Frontiers in Microbiology</i> , 2020, 11, 581610.	3.5	12
23	Multilocus sequence typing of a dairy-associated <i>Leuconostoc mesenteroides</i> population reveals clonal structure with intragenic homologous recombination. <i>Journal of Dairy Science</i> , 2015, 98, 2284-2293.	3.4	11
24	Effect of different calcium salts and methods for triggering gelation on the characteristics of microencapsulated <i>Lactobacillus plantarum</i> LIP-1. <i>RSC Advances</i> , 2015, 5, 73352-73362.	3.6	11
25	Bacterial composition and function during fermentation of Mongolia koumiss. <i>Food Science and Nutrition</i> , 2021, 9, 4146-4155.	3.4	11
26	Metabolomic analysis of significant changes in <i>Lactobacillus casei</i> Zhang during culturing to generation 4,000 under conditions of glucose restriction. <i>Journal of Dairy Science</i> , 2019, 102, 3851-3867.	3.4	9
27	A survey of the relationship between functional genes and acetaldehyde production characteristics in <i>Streptococcus thermophilus</i> by multilocus sequence typing. <i>Journal of Dairy Science</i> , 2019, 102, 9651-9662.	3.4	8
28	Evaluation of Bacterial Contamination in Goat Milk Powder Using PacBio Single Molecule Real-Time Sequencing and Droplet Digital PCR. <i>Journal of Food Protection</i> , 2018, 81, 1791-1799.	1.7	3