

Bilige Menghe

List of Publications by Year in descending order

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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	Bacterial composition and function during fermentation of Mongolia koumiss. Food Science and Nutrition, 2021, 9, 4146-4155.	3.4	11
2	Comparison of Bacterial Microbiota in Raw Mare's Milk and Koumiss Using PacBio Single Molecule Real-Time Sequencing Technology. Frontiers in Microbiology, 2020, 11, 581610.	3.5	12
3	Characterization of potentially probiotic lactic acid bacteria and bifidobacteria isolated from human colostrum. Journal of Dairy Science, 2020, 103, 4013-4025.	3.4	75
4	Profiling of koumiss microbiota and organic acids and their effects on koumiss taste. BMC Microbiology, 2020, 20, 85.	3.3	37
5	Metabolomic analysis of significant changes in <i>Lactobacillus casei</i> Zhang during culturing to generation 4,000 under conditions of glucose restriction. Journal of Dairy Science, 2019, 102, 3851-3867.	3.4	9
6	A survey of the relationship between functional genes and acetaldehyde production characteristics in <i>Streptococcus thermophilus</i> by multilocus sequence typing. Journal of Dairy Science, 2019, 102, 9651-9662.	3.4	8
7	Evaluation of Bacterial Contamination in Goat Milk Powder Using PacBio Single Molecule Real-Time Sequencing and Droplet Digital PCR. Journal of Food Protection, 2018, 81, 1791-1799.	1.7	3
8	A Metabolomics Approach Uncovers Differences between Traditional and Commercial Dairy Products in Buryatia (Russian Federation). Molecules, 2018, 23, 735.	3.8	24
9	Characterization of Antibiotic Resistance Genes from <i>Lactobacillus</i> Isolated from Traditional Dairy Products. Journal of Food Science, 2017, 82, 724-730.	3.1	111
10	Comparative genomic analysis of the genus <i>Enterococcus</i> . Microbiological Research, 2017, 196, 95-105.	5.3	53
11	Effects of microencapsulated <i>Lactobacillus plantarum</i> LIP-1 on the gut microbiota of hyperlipidaemic rats. British Journal of Nutrition, 2017, 118, 481-492.	2.3	79
12	A Perspective Study of Koumiss Microbiome by Metagenomics Analysis Based on Single-Cell Amplification Technique. Frontiers in Microbiology, 2017, 8, 165.	3.5	50
13	Carbohydrate Staple Food Modulates Gut Microbiota of Mongolians in China. Frontiers in Microbiology, 2017, 8, 484.	3.5	40
14	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. Korean Journal for Food Science of Animal Resources, 2016, 36, 499-507.	1.5	30
15	Multilocus sequence typing of <i>Lactobacillus casei</i> isolates from naturally fermented foods in China and Mongolia. Journal of Dairy Science, 2016, 99, 5202-5213.	3.4	27
16	Investigating bacterial population structure and dynamics in traditional koumiss from Inner Mongolia using single molecule real-time sequencing. Journal of Dairy Science, 2016, 99, 7852-7863.	3.4	40
17	Genetic diversity and population structure of <i>Lactobacillus delbrueckii</i> subspecies <i>bulgaricus</i> isolated from naturally fermented dairy foods. Scientific Reports, 2016, 6, 22704.	3.3	16
18	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. Journal of Dairy Science, 2016, 99, 89-103.	3.4	28

#	ARTICLE	IF	CITATIONS
19	Comparative Genomic Analysis of 45 Type Strains of the Genus Bifidobacterium: A Snapshot of Its Genetic Diversity and Evolution. PLoS ONE, 2015, 10, e0117912.	2.5	90
20	Multilocus sequence typing of Streptococcus thermophilus from naturally fermented dairy foods in China and Mongolia. BMC Microbiology, 2015, 15, 236.	3.3	52
21	A phylo-functional core of gut microbiota in healthy young Chinese cohorts across lifestyles, geography and ethnicities. ISME Journal, 2015, 9, 1979-1990.	9.8	339
22	Multilocus sequence typing of a dairy-associated Leuconostoc mesenteroides population reveals clonal structure with intragenic homologous recombination. Journal of Dairy Science, 2015, 98, 2284-2293.	3.4	11
23	Short communication: Single molecule, real-time sequencing technology revealed species- and strain-specific methylation patterns of 2 Lactobacillus strains. Journal of Dairy Science, 2015, 98, 3020-3024.	3.4	38
24	The evolution and population structure of Lactobacillus fermentum from different naturally fermented products as determined by multilocus sequence typing (MLST). BMC Microbiology, 2015, 15, 107.	3.3	27
25	Effect of different calcium salts and methods for triggering gelation on the characteristics of microencapsulated Lactobacillus plantarum LIP-1. RSC Advances, 2015, 5, 73352-73362.	3.6	11
26	Multilocus sequence typing of Lactococcus lactis from naturally fermented milk foods in ethnic minority areas of China. Journal of Dairy Science, 2014, 97, 2633-2645.	3.4	24
27	Identification and characterization of the dominant lactobacilli isolated from koumiss in China. Journal of General and Applied Microbiology, 2010, 56, 257-265.	0.7	39
28	Isolation and preliminary probiotic selection of lactobacilli from koumiss in Inner Mongolia. Journal of Basic Microbiology, 2009, 49, 318-326.	3.3	119