

Michiel Kleerebezem

List of Publications by Year in descending order

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323
papers

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citations

2427
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216
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336
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336
docs citations

336
times ranked

42676
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65.	27.8	9,342
2	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	27.8	5,800
3	Richness of human gut microbiome correlates with metabolic markers. Nature, 2013, 500, 541-546.	27.8	3,641
4	An integrated catalog of reference genes in the human gut microbiome. Nature Biotechnology, 2014, 32, 834-841.	17.5	1,664
5	Complete genome sequence of <i>Lactobacillus plantarum</i> WCFS1. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1990-1995.	7.1	1,326
6	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nature Biotechnology, 2014, 32, 822-828.	17.5	909
7	Quorum sensing by peptide pheromones and two-component signal transduction systems in Gram-positive bacteria. Molecular Microbiology, 1997, 24, 895-904.	2.5	710
8	Quorum sensing-controlled gene expression in lactic acid bacteria. Journal of Biotechnology, 1998, 64, 15-21.	3.8	641
9	Emerging molecular insights into the interaction between probiotics and the host intestinal mucosa. Nature Reviews Microbiology, 2012, 10, 66-78.	28.6	557
10	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. ISME Journal, 2012, 6, 1415-1426.	9.8	544
11	Butyrate-producing <i>Clostridium</i> cluster XIVa species specifically colonize mucins in an <i>in vitro</i> gut model. ISME Journal, 2013, 7, 949-961.	9.8	501
12	10 years of the nisin-controlled gene expression system (NICE) in <i>Lactococcus lactis</i> . Applied Microbiology and Biotechnology, 2005, 68, 705-717.	3.6	498
13	Stress Physiology of Lactic Acid Bacteria. Microbiology and Molecular Biology Reviews, 2016, 80, 837-890.	6.6	487
14	Regulation of human epithelial tight junction proteins by <i>Lactobacillus plantarum</i> in vivo and protective effects on the epithelial barrier. American Journal of Physiology - Renal Physiology, 2010, 298, G851-G859.	3.4	481
15	<i>Lactobacillus plantarum</i> survival, functional and potential probiotic properties in the human intestinal tract. International Dairy Journal, 2006, 16, 1018-1028.	3.0	410
16	Differential NF- κ B pathways induction by <i>Lactobacillus plantarum</i> in the duodenum of healthy humans correlating with immune tolerance. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2371-2376.	7.1	363
17	Can probiotics modulate human disease by impacting intestinal barrier function?. British Journal of Nutrition, 2017, 117, 93-107.	2.3	343
18	Saturated fat stimulates obesity and hepatic steatosis and affects gut microbiota composition by an enhanced overflow of dietary fat to the distal intestine. American Journal of Physiology - Renal Physiology, 2012, 303, G589-G599.	3.4	330

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19	Gut microbiota facilitates dietary heme-induced epithelial hyperproliferation by opening the mucus barrier in colon. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10038-10043.	7.1	323
20	Microbiota conservation and BMI signatures in adult monozygotic twins. ISME Journal, 2013, 7, 707-717.	9.8	311
21	The extracellular biology of the lactobacilli. FEMS Microbiology Reviews, 2010, 34, 199-230.	8.6	304
22	Regulation of intestinal homeostasis and immunity with probiotic lactobacilli. Trends in Immunology, 2013, 34, 208-215.	6.8	294
23	Exopolysaccharides produced by lactic acid bacteria: from health-promoting benefits to stress tolerance mechanisms. Applied Microbiology and Biotechnology, 2016, 100, 3877-3886.	3.6	291
24	New insights in the molecular biology and physiology of revealed by comparative genomics. FEMS Microbiology Reviews, 2005, 29, 435-463.	8.6	289
25	Probiotic and Gut Lactobacilli and Bifidobacteria: Molecular Approaches to Study Diversity and Activity. Annual Review of Microbiology, 2009, 63, 269-290.	7.3	289
26	Human mucosal in vivo transcriptome responses to three lactobacilli indicate how probiotics may modulate human cellular pathways. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4562-4569.	7.1	289
27	Towards understanding molecular modes of probiotic action. Current Opinion in Biotechnology, 2006, 17, 204-210.	6.6	281
28	Biodiversity-Based Identification and Functional Characterization of the Mannose-Specific Adhesin of <i>Lactobacillus plantarum</i> . Journal of Bacteriology, 2005, 187, 6128-6136.	2.2	272
29	Microbial Community Development in a Dynamic Gut Model Is Reproducible, Colon Region Specific, and Selective for <i>Bacteroidetes</i> and <i>Clostridium</i> Cluster IX. Applied and Environmental Microbiology, 2010, 76, 5237-5246.	3.1	272
30	Phenotypic and genomic diversity of <i>Lactobacillus plantarum</i> strains isolated from various environmental niches. Environmental Microbiology, 2010, 12, 758-773.	3.8	262
31	High temporal and inter-individual variation detected in the human ileal microbiota. Environmental Microbiology, 2010, 12, 3213-3227.	3.8	254
32	Towards microbial fermentation metabolites as markers for health benefits of prebiotics. Nutrition Research Reviews, 2015, 28, 42-66.	4.1	251
33	Cell to cell communication by autoinducing peptides in gram-positive bacteria. Antonie Van Leeuwenhoek, 2002, 81, 233-243.	1.7	248
34	The impact of probiotics and prebiotics on the immune system. Nature Reviews Immunology, 2012, 12, 728-734.	22.7	247
35	Improved Vectors for Nisin-Controlled Expression in Gram-Positive Bacteria. Plasmid, 2000, 44, 183-190.	1.4	244
36	Production of Aroma Compounds in Lactic Fermentations. Annual Review of Food Science and Technology, 2014, 5, 313-326.	9.9	237

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37	Controlled gene expression systems for lactic acid bacteria: transferable nisin-inducible expression cassettes for <i>Lactococcus</i> , <i>Leuconostoc</i> , and <i>Lactobacillus</i> spp. <i>Applied and Environmental Microbiology</i> , 1997, 63, 4581-4584.	3.1	231
38	Exploring <i>Lactobacillus plantarum</i> Genome Diversity by Using Microarrays. <i>Journal of Bacteriology</i> , 2005, 187, 6119-6127.	2.2	229
39	Cofactor Engineering: a Novel Approach to Metabolic Engineering in <i>Lactococcus lactis</i> by Controlled Expression of NADH Oxidase. <i>Journal of Bacteriology</i> , 1998, 180, 3804-3808.	2.2	217
40	Arabinoxylans and inulin differentially modulate the mucosal and luminal gut microbiota and mucinâ€degradation in humanized rats. <i>Environmental Microbiology</i> , 2011, 13, 2667-2680.	3.8	215
41	Identification of <i>Lactobacillus plantarum</i> Genes That Are Induced in the Gastrointestinal Tract of Mice. <i>Journal of Bacteriology</i> , 2004, 186, 5721-5729.	2.2	211
42	Controlled overproduction of proteins by lactic acid bacteria. <i>Trends in Biotechnology</i> , 1997, 15, 135-140.	9.3	208
43	Cre- <i>lox</i> -Based System for Multiple Gene Deletions and Selectable-Marker Removal in <i>Lactobacillus plantarum</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 1126-1135.	3.1	207
44	Microbiome dynamics of human epidermis following skin barrier disruption. <i>Genome Biology</i> , 2012, 13, R101.	9.6	201
45	Temporal and spatial interplay of microbiota and intestinal mucosa drive establishment of immune homeostasis in conventionalized mice. <i>Mucosal Immunology</i> , 2012, 5, 567-579.	6.0	201
46	Quorum sensing control of lantibiotic production; nisin and subtilin autoregulate their own biosynthesis. <i>Peptides</i> , 2004, 25, 1405-1414.	2.4	198
47	Nomadic lifestyle of <i>Lactobacillus plantarum</i> revealed by comparative genomics of 54 strains isolated from different habitats. <i>Environmental Microbiology</i> , 2016, 18, 4974-4989.	3.8	197
48	Metabolic engineering of lactic acid bacteria, the combined approach: kinetic modelling, metabolic control and experimental analysis The GenBank accession number for the sequence reported in this paper is AY046926.. <i>Microbiology (United Kingdom)</i> , 2002, 148, 1003-1013.	1.8	196
49	Flavour formation from amino acids by lactic acid bacteria: predictions from genome sequence analysis. <i>International Dairy Journal</i> , 2002, 12, 111-121.	3.0	182
50	The small intestine microbiota, nutritional modulation and relevance for health. <i>Current Opinion in Biotechnology</i> , 2015, 32, 14-20.	6.6	182
51	Peptide pheromone-dependent regulation of antimicrobial peptide production in Gram-positive bacteria: a case of multicellular behavior. <i>Peptides</i> , 2001, 22, 1579-1596.	2.4	179
52	Multifactorial diversity sustains microbial community stability. <i>ISME Journal</i> , 2013, 7, 2126-2136.	9.8	176
53	Conversion of <i>Lactococcus lactis</i> from homolactic to homoalanine fermentation through metabolic engineering. <i>Nature Biotechnology</i> , 1999, 17, 588-592.	17.5	174
54	Functional Analysis of Four Bile Salt Hydrolase and Penicillin Acylase Family Members in <i>Lactobacillus plantarum</i> WCFS1. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4719-4726.	3.1	173

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55	The extracellular biology of the lactobacilli. FEMS Microbiology Reviews, 2010, 34, 199-230.	8.6	173
56	Involvement of stress protein PspA (phage shock protein A) of Escherichia coli in maintenance of the protonmotive force under stress conditions.. EMBO Journal, 1996, 15, 162-171.	7.8	172
57	Use of the Lactococcal <i>nisA</i> Promoter To Regulate Gene Expression in Gram-Positive Bacteria: Comparison of Induction Level and Promoter Strength. Applied and Environmental Microbiology, 1998, 64, 2763-2769.	3.1	171
58	Isolation of DNA from bacterial samples of the human gastrointestinal tract. Nature Protocols, 2006, 1, 870-873.	12.0	171
59	Identification of Genetic Loci in Lactobacillus plantarum That Modulate the Immune Response of Dendritic Cells Using Comparative Genome Hybridization. PLoS ONE, 2010, 5, e10632.	2.5	170
60	Increased Production of Folate by Metabolic Engineering of Lactococcus lactis. Applied and Environmental Microbiology, 2003, 69, 3069-3076.	3.1	169
61	<i>Lactococcus lactis</i> as a Cell Factory for High-Level Diacetyl Production. Applied and Environmental Microbiology, 2000, 66, 4112-4114.	3.1	168
62	Discovering lactic acid bacteria by genomics. Antonie Van Leeuwenhoek, 2002, 82, 29-58.	1.7	164
63	Identification of Lactobacillus plantarum genes modulating the cytokine response of human peripheral blood mononuclear cells. BMC Microbiology, 2010, 10, 293.	3.3	162
64	Comparative analysis of proteins with a mucus-binding domain found exclusively in lactic acid bacteria. Microbiology (United Kingdom), 2006, 152, 273-280.	1.8	155
65	Microbial domestication signatures of <i>Lactococcus lactis</i> can be reproduced by experimental evolution. Genome Research, 2012, 22, 115-124.	5.5	154
66	Complete Sequences of Four Plasmids of Lactococcus lactis subsp. cremoris SK11 Reveal Extensive Adaptation to the Dairy Environment. Applied and Environmental Microbiology, 2005, 71, 8371-8382.	3.1	150
67	Adaptation of the Nisin-Controlled Expression System in <i>Lactobacillus plantarum</i> : a Tool To Study In Vivo Biological Effects. Applied and Environmental Microbiology, 2000, 66, 4427-4432.	3.1	147
68	An agr -Like Two-Component Regulatory System in Lactobacillus plantarum Is Involved in Production of a Novel Cyclic Peptide and Regulation of Adherence. Journal of Bacteriology, 2005, 187, 5224-5235.	2.2	144
69	Microarray Analysis and Barcoded Pyrosequencing Provide Consistent Microbial Profiles Depending on the Source of Human Intestinal Samples. Applied and Environmental Microbiology, 2011, 77, 2071-2080.	3.1	141
70	DNA micro-array-based identification of bile-responsive genes in Lactobacillus plantarum. Journal of Applied Microbiology, 2006, 100, 728-738.	3.1	139
71	Metabolic pathway engineering in lactic acid bacteria. Current Opinion in Biotechnology, 2003, 14, 232-237.	6.6	138
72	Microbiome and skin diseases. Current Opinion in Allergy and Clinical Immunology, 2013, 13, 514-520.	2.3	138

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73	Metabolic Engineering of Acetaldehyde Production by <i>Streptococcus thermophilus</i> . Applied and Environmental Microbiology, 2002, 68, 5656-5662.	3.1	134
74	Genome-Wide Detection and Analysis of Cell Wall-Bound Proteins with LPxTG-Like Sorting Motifs. Journal of Bacteriology, 2005, 187, 4928-4934.	2.2	134
75	On the ecosystemic network of saliva in healthy young adults. ISME Journal, 2017, 11, 1218-1231.	9.8	132
76	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. Microbiome, 2017, 5, 43.	11.1	132
77	Genetic Characterization of the Bile Salt Response in <i>Lactobacillus plantarum</i> and Analysis of Responsive Promoters In Vitro and In Situ in the Gastrointestinal Tract. Journal of Bacteriology, 2004, 186, 7829-7835.	2.2	130
78	H ₂ O ₂ Production in Species of the <i>Lactobacillus acidophilus</i> Group: a Central Role for a Novel NADH-Dependent Flavin Reductase. Applied and Environmental Microbiology, 2014, 80, 2229-2239.	3.1	130
79	Regulation of Exopolysaccharide Production by <i>Lactococcus lactis</i> subsp. <i>cremoris</i> by the Sugar Source. Applied and Environmental Microbiology, 1999, 65, 5003-5008.	3.1	122
80	Diversity of human small intestinal <i>Streptococcus</i> and <i>Veillonella</i> populations. FEMS Microbiology Ecology, 2013, 85, 376-388.	2.7	121
81	The gut microbiota elicits a profound metabolic reorientation in the mouse jejunal mucosa during conventionalisation. Gut, 2013, 62, 1306-1314.	12.1	118
82	Immunomodulatory Properties of <i>Streptococcus</i> and <i>Veillonella</i> Isolates from the Human Small Intestine Microbiota. PLoS ONE, 2014, 9, e114277.	2.5	118
83	Sugar catabolism and its impact on the biosynthesis and engineering of exopolysaccharide production in lactic acid bacteria. International Dairy Journal, 2001, 11, 723-732.	3.0	117
84	Functional Analysis of the <i>Lactococcus lactis</i> galU and galE Genes and Their Impact on Sugar Nucleotide and Exopolysaccharide Biosynthesis. Applied and Environmental Microbiology, 2001, 67, 3033-3040.	3.1	117
85	Microbial communities in the human small intestine: coupling diversity to metagenomics. Future Microbiology, 2007, 2, 285-295.	2.0	117
86	Characterization of a locus from <i>Carnobacterium piscicola</i> LV17B involved in bacteriocin production and immunity: evidence for global inducer-mediated transcriptional regulation. Journal of Bacteriology, 1997, 179, 6163-6171.	2.2	116
87	Intestinal colonisation patterns in breastfed and formula-fed infants during the first 12 weeks of life reveal sequential microbiota signatures. Scientific Reports, 2017, 7, 8327.	3.3	115
88	Metabolic engineering of lactic acid bacteria for the production of nutraceuticals. Antonie Van Leeuwenhoek, 2002, 82, 217-235.	1.7	112
89	Control of Lactose Transport, β -Galactosidase Activity, and Glycolysis by CcpA in <i>Streptococcus thermophilus</i> : Evidence for Carbon Catabolite Repression by a Non-Phosphoenolpyruvate-Dependent Phosphotransferase System Sugar. Journal of Bacteriology, 2000, 182, 5982-5989.	2.2	111
90	A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. BMC Genomics, 2013, 14, 530.	2.8	111

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91	The gut microbiota and mucosal homeostasis. Gut Microbes, 2013, 4, 118-124.	9.8	111
92	Complete Resequencing and Reannotation of the Lactobacillus plantarum WCFS1 Genome. Journal of Bacteriology, 2012, 194, 195-196.	2.2	109
93	High-Level Production of the Low-Calorie Sugar Sorbitol by Lactobacillus plantarum through Metabolic Engineering. Applied and Environmental Microbiology, 2007, 73, 1864-1872.	3.1	108
94	In vivo nuclear magnetic resonance studies of glycolytic kinetics in Lactococcus lactis. , 1999, 64, 200-212.		107
95	Spatial and Temporal Expression of Lactobacillus plantarum Genes in the Gastrointestinal Tracts of Mice. Applied and Environmental Microbiology, 2007, 73, 124-132.	3.1	107
96	Title is missing!. Antonie Van Leeuwenhoek, 1999, 76, 357-365.	1.7	105
97	Improvement of an experimental colitis in rats by lactic acid bacteria producing superoxide dismutase. Inflammatory Bowel Diseases, 2006, 12, 1044-1052.	1.9	104
98	The complete genomes of Lactobacillus plantarum and Lactobacillus johnsonii reveal extensive differences in chromosome organization and gene content. Microbiology (United Kingdom), 2004, 150, 3601-3611.	1.8	103
99	Strain-Specific Features of Extracellular Polysaccharides and Their Impact on Lactobacillus plantarum-Host Interactions. Applied and Environmental Microbiology, 2016, 82, 3959-3970.	3.1	102
100	Functional Analysis of Three Plasmids from Lactobacillus plantarum. Applied and Environmental Microbiology, 2005, 71, 1223-1230.	3.1	100
101	New insights in the molecular biology and physiology of <i>Streptococcus thermophilus</i> revealed by comparative genomics. FEMS Microbiology Reviews, 2005, 29, 435-463.	8.6	99
102	Lifestyle of <i>Lactobacillus plantarum</i> in the mouse caecum. Environmental Microbiology, 2009, 11, 2747-2757.	3.8	99
103	Dietary Heme Alters Microbiota and Mucosa of Mouse Colon without Functional Changes in Host-Microbe Cross-Talk. PLoS ONE, 2012, 7, e49868.	2.5	99
104	Involvement of stress protein PspA (phage shock protein A) of Escherichia coli in maintenance of the protonmotive force under stress conditions. EMBO Journal, 1996, 15, 162-71.	7.8	99
105	Metabolic engineering of lactic acid bacteria: overview of the approaches and results of pathway rerouting involved in food fermentations. Current Opinion in Biotechnology, 1999, 10, 492-497.	6.6	98
106	Lactobacillus plantarum gene clusters encoding putative cell-surface protein complexes for carbohydrate utilization are conserved in specific gram-positive bacteria. BMC Genomics, 2006, 7, 126.	2.8	96
107	Short- and Long-Term Adaptation to Ethanol Stress and Its Cross-Protective Consequences in Lactobacillus plantarum. Applied and Environmental Microbiology, 2011, 77, 5247-5256.	3.1	96
108	Impact of 4 Lactobacillus plantarum capsular polysaccharide clusters on surface glycan composition and host cell signaling. Microbial Cell Factories, 2012, 11, 149.	4.0	96

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109	Functional Analysis of Glycosyltransferase Genes from <i>Lactococcus lactis</i> and Other Gram-Positive Cocci: Complementation, Expression, and Diversity. <i>Journal of Bacteriology</i> , 1999, 181, 6347-6353.	2.2	96
110	The predicted secretome of <i>Lactobacillus plantarum</i> WCFS1 sheds light on interactions with its environment. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3175-3183.	1.8	95
111	Convergence in probiotic <i>Lactobacillus</i> gut-adaptive responses in humans and mice. <i>ISME Journal</i> , 2010, 4, 1481-1484.	9.8	95
112	Development and Characterization of a Subtilin-Regulated Expression System in <i>Bacillus subtilis</i> : Strict Control of Gene Expression by Addition of Subtilin. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8818-8824.	3.1	93
113	Functional implications of the microbial community structure of undefined mesophilic starter cultures. <i>Microbial Cell Factories</i> , 2014, 13, S2.	4.0	93
114	Genetics and engineering of microbial exopolysaccharides for food: approaches for the production of existing and novel polysaccharides. <i>Current Opinion in Biotechnology</i> , 1999, 10, 498-504.	6.6	92
115	Lactate racemase is a nickel-dependent enzyme activated by a widespread maturation system. <i>Nature Communications</i> , 2014, 5, 3615.	12.8	91
116	The quest for probiotic effector molecules—Unraveling strain specificity at the molecular level. <i>Pharmacological Research</i> , 2013, 69, 61-74.	7.1	88
117	Dehydration and thermal inactivation of <i>Lactobacillus plantarum</i> WCFS1: Comparing single droplet drying to spray and freeze drying. <i>Food Research International</i> , 2013, 54, 1351-1359.	6.2	87
118	Use of the <i>alr</i> Gene as a Food-Grade Selection Marker in Lactic Acid Bacteria. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5663-5670.	3.1	85
119	Characterization and Functional Analysis of the <i>poxB</i> Gene, Which Encodes Pyruvate Oxidase in <i>Lactobacillus plantarum</i> . <i>Journal of Bacteriology</i> , 2004, 186, 3749-3759.	2.2	85
120	High-Level Acetaldehyde Production in <i>Lactococcus lactis</i> by Metabolic Engineering. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1109-1113.	3.1	84
121	Gut bacteria—host metabolic interplay during conventionalisation of the mouse germfree colon. <i>ISME Journal</i> , 2013, 7, 743-755.	9.8	84
122	Influence of fermented milk products, prebiotics and probiotics on microbiota composition and health. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2013, 27, 139-155.	2.4	83
123	Effect of Different NADH Oxidase Levels on Glucose Metabolism by <i>Lactococcus lactis</i> : Kinetics of Intracellular Metabolite Pools Determined by In Vivo Nuclear Magnetic Resonance. <i>Applied and Environmental Microbiology</i> , 2002, 68, 6332-6342.	3.1	82
124	Isolation of RNA from bacterial samples of the human gastrointestinal tract. <i>Nature Protocols</i> , 2006, 1, 954-959.	12.0	82
125	Role of the carboxy-terminal phenylalanine in the biogenesis of outer membrane protein PhoE of <i>Escherichia coli</i> K-12. <i>Journal of Molecular Biology</i> , 1997, 269, 473-478.	4.2	81
126	Lactate Racemization as a Rescue Pathway for Supplying d -Lactate to the Cell Wall Biosynthesis Machinery in <i>Lactobacillus plantarum</i> . <i>Journal of Bacteriology</i> , 2005, 187, 6750-6761.	2.2	81

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127	Fluorescence and Atomic Force Microscopy Imaging of Wall Teichoic Acids in <i>Lactobacillus plantarum</i> . ACS Chemical Biology, 2011, 6, 366-376.	3.4	80
128	Sialyllactose and Galactooligosaccharides Promote Epithelial Barrier Functioning and Distinctly Modulate Microbiota Composition and Short Chain Fatty Acid Production In Vitro. Frontiers in Immunology, 2019, 10, 94.	4.8	80
129	Expression of the <i>pspA</i> gene stimulates efficient protein export in <i>Escherichia coli</i> . Molecular Microbiology, 1993, 7, 947-956.	2.5	79
130	Regulation of the <i>metC-cysK</i> Operon, Involved in Sulfur Metabolism in <i>Lactococcus lactis</i> . Journal of Bacteriology, 2002, 184, 82-90.	2.2	79
131	Recombinant lactic acid bacteria as mucosal biotherapeutic agents. Trends in Biotechnology, 2011, 29, 499-508.	9.3	79
132	Metatranscriptome Analysis of the Human Fecal Microbiota Reveals Subject-Specific Expression Profiles, with Genes Encoding Proteins Involved in Carbohydrate Metabolism Being Dominantly Expressed. Applied and Environmental Microbiology, 2010, 76, 5533-5540.	3.1	76
133	Discovering lactic acid bacteria by genomics. , 2002, 82, 29-58.		74
134	Making sense of quorum sensing in lactobacilli: a special focus on <i>Lactobacillus plantarum</i> WCFS1. Microbiology (United Kingdom), 2007, 153, 3939-3947.	1.8	74
135	Evolutionary engineering to enhance starter culture performance in food fermentations. Current Opinion in Biotechnology, 2015, 32, 1-7.	6.6	74
136	Exopolysaccharide Biosynthesis in <i>Lactococcus lactis</i> NIZO B40: Functional Analysis of the Glycosyltransferase Genes Involved in Synthesis of the Polysaccharide Backbone. Journal of Bacteriology, 1999, 181, 338-340.	2.2	74
137	Visualisation of dCas9 target search in vivo using an open-microscopy framework. Nature Communications, 2019, 10, 3552.	12.8	70
138	Identification of the transcriptional response of human intestinal mucosa to <i>Lactobacillus plantarum</i> WCFS1 in vivo. BMC Genomics, 2008, 9, 374.	2.8	69
139	IS 981 -Mediated Adaptive Evolution Recovers Lactate Production by <i>ldhB</i> Transcription Activation in a Lactate Dehydrogenase-Deficient Strain of <i>Lactococcus lactis</i> . Journal of Bacteriology, 2003, 185, 4499-4507.	2.2	68
140	Genome-based in silico detection of putative manganese transport systems in <i>Lactobacillus plantarum</i> and their genetic analysis. Microbiology (United Kingdom), 2005, 151, 1229-1238.	1.8	68
141	Potential and Opportunities for Use of Recombinant Lactic Acid Bacteria in Human Health. Advances in Applied Microbiology, 2004, 56, 1-64.	2.4	67
142	Major Role of NAD-Dependent Lactate Dehydrogenases in Aerobic Lactate Utilization in <i>Lactobacillus plantarum</i> during Early Stationary Phase. Journal of Bacteriology, 2004, 186, 6661-6666.	2.2	66
143	d-Alanyl Ester Depletion of Teichoic Acids in <i>Lactobacillus plantarum</i> Results in a Major Modification of Lipoteichoic Acid Composition and Cell Wall Perforations at the Septum Mediated by the <i>Acm2</i> Autolysin. Journal of Bacteriology, 2006, 188, 3709-3715.	2.2	66
144	Cell surface-associated compounds of probiotic lactobacilli sustain the strain-specificity dogma. Current Opinion in Microbiology, 2013, 16, 262-269.	5.1	66

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145	The prophage sequences of <i>Lactobacillus plantarum</i> strain WCFS1. <i>Virology</i> , 2003, 316, 245-255.	2.4	65
146	Involvement of Pyruvate Oxidase Activity and Acetate Production in the Survival of <i>Lactobacillus plantarum</i> during the Stationary Phase of Aerobic Growth. <i>Applied and Environmental Microbiology</i> , 2006, 72, 7933-7940.	3.1	64
147	Transient inflammatory-like state and microbial dysbiosis are pivotal in establishment of mucosal homeostasis during colonisation of germ-free mice. <i>Beneficial Microbes</i> , 2014, 5, 67-77.	2.4	64
148	Genome data mining of lactic acid bacteria: the impact of bioinformatics. <i>Current Opinion in Biotechnology</i> , 2004, 15, 105-115.	6.6	63
149	Genome Sequence of the Naturally Plasmid-Free <i>Lactobacillus plantarum</i> Strain NC8 (CCUG 61730). <i>Journal of Bacteriology</i> , 2012, 194, 2391-2392.	2.2	61
150	Intestinal colonization: How key microbial players become established in this dynamic process. <i>BioEssays</i> , 2013, 35, 913-923.	2.5	61
151	The human gut microbiome: are we our enterotypes?. <i>Microbial Biotechnology</i> , 2011, 4, 550-553.	4.2	59
152	The microbiota and the gut-brain axis: insights from the temporal and spatial mucosal alterations during colonisation of the germfree mouse intestine. <i>Beneficial Microbes</i> , 2012, 3, 251-259.	2.4	59
153	Engineering of Carbon Distribution between Glycolysis and Sugar Nucleotide Biosynthesis in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2003, 69, 1129-1135.	3.1	58
154	The <i>Lactobacillus plantarum</i> ftsH Gene Is a Novel Member of the CtsR Stress Response Regulon. <i>Journal of Bacteriology</i> , 2009, 191, 1688-1694.	2.2	58
155	Comparative Genomics Analysis of <i>Streptococcus</i> Isolates from the Human Small Intestine Reveals their Adaptation to a Highly Dynamic Ecosystem. <i>PLoS ONE</i> , 2013, 8, e83418.	2.5	57
156	Gram-positive anaerobe cocci are underrepresented in the microbiome of filaggrin-deficient human skin. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 1368-1371.	2.9	57
157	Identification and Genetic Characterization of a Novel Proteinase, PrtR, from the Human Isolate <i>Lactobacillus rhamnosus</i> BCT10. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5802-5811.	3.1	56
158	Modulation of <i>Lactobacillus plantarum</i> Gastrointestinal Robustness by Fermentation Conditions Enables Identification of Bacterial Robustness Markers. <i>PLoS ONE</i> , 2012, 7, e39053.	2.5	56
159	Engineering lactic acid bacteria for increased industrial functionality. <i>Bioengineered Bugs</i> , 2011, 2, 80-87.	1.7	55
160	Effect of a long-term high-protein diet on survival, obesity development, and gut microbiota in mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2016, 310, E886-E899.	3.5	55
161	Understanding mode of action can drive the translational pipeline towards more reliable health benefits for probiotics. <i>Current Opinion in Biotechnology</i> , 2019, 56, 55-60.	6.6	55
162	Increased Exopolysaccharide Production in <i>Lactococcus lactis</i> due to Increased Levels of Expression of the NIZO B40 eps Gene Cluster. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5029-5031.	3.1	53

#	ARTICLE	IF	CITATIONS
163	Post-genomics of lactic acid bacteria and other food-grade bacteria to discover gut functionality. <i>Current Opinion in Biotechnology</i> , 2004, 15, 86-93.	6.6	53
164	The Variable Regions of <i>Lactobacillus rhamnosus</i> Genomes Reveal the Dynamic Evolution of Metabolic and Host-Adaptation Repertoires. <i>Genome Biology and Evolution</i> , 2016, 8, 1889-1905.	2.5	53
165	Nucleotide Sequence Analysis of the Lactococcal EPS Plasmid pNZ4000. <i>Plasmid</i> , 2000, 43, 130-136.	1.4	52
166	T lymphocytes control microbial composition by regulating the abundance of <i>Vibrio</i> in the zebrafish gut. <i>Gut Microbes</i> , 2014, 5, 737-747.	9.8	51
167	Perspective: Fundamental Limitations of the Randomized Controlled Trial Method in Nutritional Research: The Example of Probiotics. <i>Advances in Nutrition</i> , 2018, 9, 561-571.	6.4	51
168	<i>Lactobacillus plantarum</i> possesses the capability for wall teichoic acid backbone alditol switching. <i>Microbial Cell Factories</i> , 2012, 11, 123.	4.0	50
169	Transcriptomes Reveal Genetic Signatures Underlying Physiological Variations Imposed by Different Fermentation Conditions in <i>Lactobacillus plantarum</i> . <i>PLoS ONE</i> , 2012, 7, e38720.	2.5	50
170	Mining microbial metatranscriptomes for expression of antibiotic resistance genes under natural conditions. <i>Scientific Reports</i> , 2015, 5, 11981.	3.3	50
171	Use of propidium monoazide for selective profiling of viable microbial cells during Gouda cheese ripening. <i>International Journal of Food Microbiology</i> , 2016, 228, 1-9.	4.7	50
172	Human milk extracellular vesicles target nodes in interconnected signalling pathways that enhance oral epithelial barrier function and dampen immune responses. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12071.	12.2	50
173	Improvement of <i>Lactobacillus plantarum</i> Aerobic Growth as Directed by Comprehensive Transcriptome Analysis. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4776-4778.	3.1	49
174	Expression systems for industrial Gram-positive bacteria with low guanine and cytosine content. <i>Current Opinion in Biotechnology</i> , 1997, 8, 547-553.	6.6	48
175	Acetate Utilization in <i>Lactococcus lactis</i> Deficient in Lactate Dehydrogenase: a Rescue Pathway for Maintaining Redox Balance. <i>Journal of Bacteriology</i> , 1999, 181, 5521-5526.	2.2	48
176	High local substrate availability stabilizes a cooperative trait. <i>ISME Journal</i> , 2011, 5, 929-932.	9.8	47
177	The Impact of <i>Lactobacillus plantarum</i> WCFS1 Teichoic Acid D-Alanylation on the Generation of Effector and Regulatory T-cells in Healthy Mice. <i>PLoS ONE</i> , 2013, 8, e63099.	2.5	47
178	Sugar Utilisation and Conservation of the gal-lac Gene Cluster in <i>Streptococcus thermophilus</i> . <i>Systematic and Applied Microbiology</i> , 2004, 27, 10-17.	2.8	46
179	Correlation of <i>Lactobacillus rhamnosus</i> Genotypes and Carbohydrate Utilization Signatures Determined by Phenotype Profiling. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5458-5470.	3.1	46
180	IL-22-STAT3 Pathway Plays a Key Role in the Maintenance of Ileal Homeostasis in Mice Lacking Secreted Mucus Barrier. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 531-542.	1.9	46

#	ARTICLE	IF	CITATIONS
181	An in silico analysis of T-box regulated genes and T-box evolution in prokaryotes, with emphasis on prediction of substrate specificity of transporters. BMC Genomics, 2008, 9, 330.	2.8	45
182	Identification of key peptidoglycan hydrolases for morphogenesis, autolysis, and peptidoglycan composition of <i>Lactobacillus plantarum</i> WCFS1. Microbial Cell Factories, 2012, 11, 137.	4.0	45
183	Characterization of an <i>Escherichia coli</i> rotA mutant, affected in periplasmic peptidylprolyl cis/trans isomerase. Molecular Microbiology, 1995, 18, 313-320.	2.5	44
184	Reply to Meisel et al.. Journal of Investigative Dermatology, 2017, 137, 961-962.	0.7	43
185	Versatile Cas9-Driven Subpopulation Selection Toolbox for <i>Lactococcus lactis</i> . Applied and Environmental Microbiology, 2018, 84, .	3.1	43
186	Controlled Modulation of Folate Polyglutamyl Tail Length by Metabolic Engineering of <i>Lactococcus lactis</i> . Applied and Environmental Microbiology, 2003, 69, 7101-7107.	3.1	42
187	O-Glycosylation as a Novel Control Mechanism of Peptidoglycan Hydrolase Activity. Journal of Biological Chemistry, 2013, 288, 22233-22247.	3.4	42
188	Physiological and Transcriptional Responses of Different Industrial Microbes at Near-Zero Specific Growth Rates. Applied and Environmental Microbiology, 2015, 81, 5662-5670.	3.1	42
189	Predicting cis-acting elements of <i>Lactobacillus plantarum</i> by comparative genomics with different taxonomic subgroups. Nucleic Acids Research, 2006, 34, 1947-1958.	14.5	41
190	Assessment of real-time RT-PCR for quantification of <i>Lactobacillus plantarum</i> gene expression during stationary phase and nutrient starvation. Journal of Applied Microbiology, 2008, 104, 587-594.	3.1	41
191	Biodiversity of mannose-specific adhesion in <i>Lactobacillus plantarum</i> revisited: strain-specific domain composition of the mannose-adhesin. Beneficial Microbes, 2010, 1, 61-66.	2.4	41
192	Comparison of the effects of five dietary fibers on mucosal transcriptional profiles, and luminal microbiota composition and SCFA concentrations in murine colon. Molecular Nutrition and Food Research, 2015, 59, 1590-1602.	3.3	41
193	Identification and Functional Characterization of the <i>Lactococcus lactis</i> rfb Operon, Required for dTDP-Rhamnose Biosynthesis. Journal of Bacteriology, 2004, 186, 1239-1248.	2.2	40
194	Mannose-specific interaction of <i>Lactobacillus plantarum</i> with porcine jejunal epithelium. FEMS Immunology and Medical Microbiology, 2008, 54, 215-223.	2.7	40
195	An intimate relationship: How probiotic lactobacilli communicate with the host. European Journal of Pharmacology, 2011, 668, S33-S42.	3.5	40
196	Autoregulation of subtilin biosynthesis in <i>Bacillus subtilis</i> : the role of the spa-box in subtilin-responsive promoters. Peptides, 2004, 25, 1415-1424.	2.4	39
197	Improved annotation of conjugated bile acid hydrolase superfamily members in Gram-positive bacteria. Microbiology (United Kingdom), 2008, 154, 2492-2500.	1.8	39
198	A high-throughput cheese manufacturing model for effective cheese starter culture screening. Journal of Dairy Science, 2009, 92, 5868-5882.	3.4	38

#	ARTICLE	IF	CITATIONS
199	Strain-specific immunomodulatory effects of <i>Lactobacillus plantarum</i> strains on birch-pollen-allergic subjects out of season. <i>Clinical and Experimental Allergy</i> , 2011, 41, 232-242.	2.9	38
200	Selection and Characterization of Conditionally Active Promoters in <i>Lactobacillus plantarum</i> , Using Alanine Racemase as a Promoter Probe. <i>Applied and Environmental Microbiology</i> , 2004, 70, 310-317.	3.1	37
201	Involvement of the Mannose Phosphotransferase System of <i>Lactobacillus plantarum</i> WCFS1 in Peroxide Stress Tolerance. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3748-3752.	3.1	37
202	The Major Autolysin Acm2 from <i>Lactobacillus plantarum</i> Undergoes Cytoplasmic O-Glycosylation. <i>Journal of Bacteriology</i> , 2012, 194, 325-333.	2.2	37
203	Impact of <i>Lactobacillus plantarum</i> Sortase on Target Protein Sorting, Gastrointestinal Persistence, and Host Immune Response Modulation. <i>Journal of Bacteriology</i> , 2013, 195, 502-509.	2.2	37
204	Dynamics of competitive population abundance of <i>Lactobacillus plantarum</i> <i>ivi</i> gene mutants in faecal samples after passage through the gastrointestinal tract of mice. <i>Journal of Applied Microbiology</i> , 2007, 103, 1424-1434.	3.1	36
205	Renaissance of traditional DNA transfer strategies for improvement of industrial lactic acid bacteria. <i>Current Opinion in Biotechnology</i> , 2019, 56, 61-68.	6.6	36
206	Early life feeding accelerates gut microbiome maturation and suppresses acute post-weaning stress in piglets. <i>Environmental Microbiology</i> , 2021, 23, 7201-7213.	3.8	36
207	Two Homologous Agr-Like Quorum-Sensing Systems Cooperatively Control Adherence, Cell Morphology, and Cell Viability Properties in <i>Lactobacillus plantarum</i> WCFS1. <i>Journal of Bacteriology</i> , 2008, 190, 7655-7665.	2.2	34
208	Modulation of the microbial fermentation in the gut by fermentable carbohydrates. <i>Bioactive Carbohydrates and Dietary Fibre</i> , 2013, 2, 133-142.	2.7	34
209	Dietary calcium phosphate strongly impacts gut microbiome changes elicited by inulin and galacto-oligosaccharides consumption. <i>Microbiome</i> , 2021, 9, 218.	11.1	32
210	A two-component signal-transduction cascade in <i>Carnobacterium piscicola</i> LV17B: two signaling peptides and one sensor-transmitter. <i>Peptides</i> , 2001, 22, 1597-1601.	2.4	31
211	Molecular characterization of the CmbR activator-binding site in the <i>metC-cysK</i> promoter region in <i>Lactococcus lactis</i> . <i>Microbiology (United Kingdom)</i> , 2005, 151, 439-446.	1.8	31
212	Introducing glutathione biosynthetic capability into <i>Lactococcus lactis</i> subsp. <i>cremoris</i> NZ9000 improves the oxidative-stress resistance of the host. <i>Metabolic Engineering</i> , 2006, 8, 662-671.	7.0	31
213	Time-resolved genetic responses of <i>Lactococcus lactis</i> to a dairy environment. <i>Environmental Microbiology</i> , 2010, 12, 1260-1270.	3.8	31
214	Volatile sulphur compounds in morning breath of human volunteers. <i>Archives of Oral Biology</i> , 2011, 56, 29-34.	1.8	31
215	Lactic Acid Bacteria for Delivery of Endogenous or Engineered Therapeutic Molecules. <i>Frontiers in Microbiology</i> , 2018, 9, 1821.	3.5	31
216	Congruent Strain Specific Intestinal Persistence of <i>Lactobacillus plantarum</i> in an Intestine-Mimicking In Vitro System and in Human Volunteers. <i>PLoS ONE</i> , 2012, 7, e44588.	2.5	31

#	ARTICLE	IF	CITATIONS
217	In Vitro Analysis of Protection of the Enzyme Bile Salt Hydrolase against Enteric Conditions by Whey Proteinâ€”Gum Arabic Microencapsulation. Journal of Agricultural and Food Chemistry, 2008, 56, 8360-8364.	5.2	30
218	Identification of Commensal Species Positively Correlated with Early Stress Responses to a Compromised Mucus Barrier. Inflammatory Bowel Diseases, 2016, 22, 826-840.	1.9	30
219	Intestinal Microbiota and Immune Modulation in Zebrafish by Fucoidan From Okinawa Mozuku (Cladosiphon okamuranus). Frontiers in Nutrition, 2020, 7, 67.	3.7	30
220	Lifestyle, metabolism and environmental adaptation in <i>Lactococcus lactis</i> . FEMS Microbiology Reviews, 2020, 44, 804-820.	8.6	29
221	Metabolic engineering of lactic acid bacteria for the production of nutraceuticals. Antonie Van Leeuwenhoek, 2002, 82, 217-35.	1.7	29
222	Metabolic engineering of <i>Lactococcus lactis</i> : the impact of genomics and metabolic modelling. Journal of Biotechnology, 2002, 98, 199-213.	3.8	28
223	Regulatory Phenotyping Reveals Important Diversity within the Species <i>Lactococcus lactis</i> . Applied and Environmental Microbiology, 2009, 75, 5687-5694.	3.1	26
224	Reconstruction of the regulatory network of <i>Lactobacillus plantarum</i> WCFS1 on basis of correlated gene expression and conserved regulatory motifs. Microbial Biotechnology, 2011, 4, 333-344.	4.2	26
225	Toward pectin fermentation by <i>Saccharomyces cerevisiae</i> : Expression of the first two steps of a bacterial pathway for d-galacturonate metabolism. Journal of Biotechnology, 2012, 162, 303-310.	3.8	26
226	Physiological and cell morphology adaptation of <i>Bacillus subtilis</i> at near-zero specific growth rates: a transcriptome analysis. Environmental Microbiology, 2015, 17, 346-363.	3.8	26
227	<i>Lactobacillus</i> strains differentially modulate cytokine production by hPBMC from pollen-allergic patients. FEMS Immunology and Medical Microbiology, 2011, 61, 28-40.	2.7	25
228	Unleashing Natural Competence in <i>Lactococcus lactis</i> by Induction of the Competence Regulator ComX. Applied and Environmental Microbiology, 2017, 83, .	3.1	25
229	High-Throughput Identification and Validation of In Situ-Expressed Genes of <i>Lactococcus lactis</i> . Applied and Environmental Microbiology, 2008, 74, 4727-4736.	3.1	24
230	Indigenous and Environmental Modulation of Frequencies of Mutation in <i>Lactobacillus plantarum</i> . Applied and Environmental Microbiology, 2010, 76, 1587-1595.	3.1	24
231	Îf 54-mediated control of the mannose phosphotransferase sytem in <i>Lactobacillus plantarum</i> impacts on carbohydrate metabolism. Microbiology (United Kingdom), 2010, 156, 695-707.	1.8	24
232	Comparative Analysis of <i>Lactobacillus plantarum</i> WCFS1 Transcriptomes by Using DNA Microarray and Next-Generation Sequencing Technologies. Applied and Environmental Microbiology, 2012, 78, 4141-4148.	3.1	24
233	Novel Method for Enumeration of Viable <i>Lactobacillus plantarum</i> WCFS1 Cells after Single-Droplet Drying. Applied and Environmental Microbiology, 2012, 78, 8082-8088.	3.1	24
234	Dietary diversity affects feeding behaviour of suckling piglets. Applied Animal Behaviour Science, 2018, 205, 151-158.	1.9	24

#	ARTICLE	IF	CITATIONS
235	Impact of early-life feeding on local intestinal microbiota and digestive system development in piglets. Scientific Reports, 2021, 11, 4213.	3.3	24
236	Synbiotic Matchmaking in <i>Lactobacillus plantarum</i> : Substrate Screening and Gene-Trait Matching To Characterize Strain-Specific Carbohydrate Utilization. Applied and Environmental Microbiology, 2020, 86, .	3.1	23
237	Functional Profiling of Unfamiliar Microbial Communities Using a Validated De Novo Assembly Metatranscriptome Pipeline. PLoS ONE, 2016, 11, e0146423.	2.5	23
238	Two Arginine Repressors Regulate Arginine Biosynthesis in <i>Lactobacillus plantarum</i> . Journal of Bacteriology, 2004, 186, 6059-6069.	2.2	22
239	The proceedings of the Tenth Symposium on Lactic Acid Bacteria. Microbial Cell Factories, 2011, 10, S1.	4.0	22
240	Omics approaches to study host-microbiota interactions. Current Opinion in Microbiology, 2013, 16, 270-277.	5.1	22
241	Making More of Milk Sugar by Engineering Lactic Acid Bacteria. International Dairy Journal, 1998, 8, 227-233.	3.0	21
242	High-Resolution Amplified Fragment Length Polymorphism Typing of <i>Lactococcus lactis</i> Strains Enables Identification of Genetic Markers for Subspecies-Related Phenotypes. Applied and Environmental Microbiology, 2011, 77, 5192-5198.	3.1	21
243	Transcriptome signatures of class I and III stress response deregulation in <i>Lactobacillus plantarum</i> reveal pleiotropic adaptation. Microbial Cell Factories, 2013, 12, 112.	4.0	21
244	Exopolysaccharides produced by <i>Lactococcus lactis</i> : from genetic engineering to improved rheological properties?. Antonie Van Leeuwenhoek, 1999, 76, 357-65.	1.7	21
245	Oxygen Relieves the CO ₂ and Acetate Dependency of <i>Lactobacillus johnsonii</i> NCC 533. PLoS ONE, 2013, 8, e57235.	2.5	20
246	GtfA and GtfB Are Both Required for Protein O-Glycosylation in <i>Lactobacillus plantarum</i> . Journal of Bacteriology, 2014, 196, 1671-1682.	2.2	20
247	Genetics of the Metabolism of Lactose and Other Sugars. , 2003, , 95-119.		20
248	Mutational analysis of the <i>Lactococcus lactis</i> NIZO B40 exopolysaccharide (EPS) gene cluster: EPS biosynthesis correlates with unphosphorylated EpsB. Journal of Applied Microbiology, 2007, 103, 2645-2656.	3.1	19
249	Genotypic adaptations associated with prolonged persistence of <i>Lactobacillus plantarum</i> in the murine digestive tract. Biotechnology Journal, 2013, 8, 895-904.	3.5	19
250	Genome-Wide Transcriptional Responses to Carbon Starvation in Nongrowing <i>Lactococcus lactis</i> . Applied and Environmental Microbiology, 2015, 81, 2554-2561.	3.1	19
251	Legitimate and Reliable Determination of the Age-Related Intestinal Microbiome in Young Piglets; Rectal Swabs and Fecal Samples Provide Comparable Insights. Frontiers in Microbiology, 2019, 10, 1886.	3.5	19
252	Comparative and functional analysis of the rRNA-operons and their tRNA gene complement in different lactic acid bacteria. Systematic and Applied Microbiology, 2006, 29, 358-367.	2.8	18

#	ARTICLE	IF	CITATIONS
253	Luciferase Detection during Stationary Phase in <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 4704-4706.	3.1	18
254	Quantitative physiology of <i>Lactococcus lactis</i> at extreme low growth rates. <i>Environmental Microbiology</i> , 2013, 15, 2319-2332.	3.8	18
255	Molecular and Metabolic Adaptations of <i>Lactococcus lactis</i> at Near-Zero Growth Rates. <i>Applied and Environmental Microbiology</i> , 2015, 81, 320-331.	3.1	18
256	Human buccal epithelium acquires microbial hyporesponsiveness at birth, a role for secretory leukocyte protease inhibitor. <i>Gut</i> , 2015, 64, 884-893.	12.1	17
257	Optimising single cell activity assessment of <i>Lactobacillus plantarum</i> by fluorescent in situ hybridisation as affected by growth. <i>Journal of Microbiological Methods</i> , 2004, 59, 109-115.	1.6	16
258	Development of the recombinase-based <i>in vivo</i> expression technology in <i>Streptococcus thermophilus</i> and validation using the lactose operon promoter. <i>Journal of Applied Microbiology</i> , 2014, 116, 620-631.	3.1	16
259	<i>Streptococcus salivarius</i> MS-oral-D6 promotes gingival re-epithelialization in vitro through a secreted serine protease. <i>Scientific Reports</i> , 2017, 7, 11100.	3.3	16
260	Microbial communities in a dynamic in vitro model for the human ileum resemble the human ileal microbiota. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	16
261	Growth, dormancy and lysis: the complex relation of starter culture physiology and cheese flavour formation. <i>Current Opinion in Food Science</i> , 2021, 39, 22-30.	8.0	16
262	Metabolic engineering of lactic acid bacteria for the production of nutraceuticals. , 2002, , 217-235.		15
263	Inactivation of <i>Lactobacillus plantarum</i> WCFS1 during spray drying and storage assessed with complementary viability determination methods. <i>Food Research International</i> , 2014, 64, 212-217.	6.2	14
264	Metatranscriptome analysis of the microbial fermentation of dietary milk proteins in the murine gut. <i>PLoS ONE</i> , 2018, 13, e0194066.	2.5	14
265	Exopolysaccharides produced by <i>Lactococcus lactis</i> : from genetic engineering to improved rheological properties?. , 1999, , 357-365.		13
266	Genome-Wide Prediction and Validation of Sigma70 Promoters in <i>Lactobacillus plantarum</i> WCFS1. <i>PLoS ONE</i> , 2012, 7, e45097.	2.5	13
267	Lipoproteins Contribute to the Anti-inflammatory Capacity of <i>Lactobacillus plantarum</i> WCFS1. <i>Frontiers in Microbiology</i> , 2020, 11, 1822.	3.5	13
268	Carbohydrate-controlled serine protease inhibitor (serpin) production in <i>Bifidobacterium longum</i> subsp. <i>longum</i> . <i>Scientific Reports</i> , 2021, 11, 7236.	3.3	13
269	Competitive Selection of Lactic Acid Bacteria That Persist in the Human Oral Cavity. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8445-8450.	3.1	12
270	Nearly Complete Genome Sequence of <i>Lactobacillus plantarum</i> Strain NIZO2877. <i>Genome Announcements</i> , 2015, 3, .	0.8	12

#	ARTICLE	IF	CITATIONS
271	A Novel Method for Long-Term Analysis of Lactic Acid and Ammonium Production in Non-growing <i>Lactococcus lactis</i> Reveals Pre-culture and Strain Dependence. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 580090.	4.1	12
272	Effects of Creep Feed Provision on Behavior and Performance of Piglets Around Weaning. <i>Frontiers in Veterinary Science</i> , 2020, 7, 520035.	2.2	12
273	Improved Efficiency and Reliability of RT-PCR Using Tag-Extended RT Primers and Temperature Gradient PCR. <i>BioTechniques</i> , 2001, 31, 466-472.	1.8	11
274	Lactic acid bacteria – Genetics, metabolism and application. <i>FEMS Microbiology Reviews</i> , 2005, 29, 391-391.	8.6	11
275	Editorial: Lactic acid bacteria – a continuing journey in science and application. <i>FEMS Microbiology Reviews</i> , 2017, 41, S1-S2.	8.6	11
276	Draft Genome Sequence of a Porcine Commensal, <i>Rothia nasimurium</i> , Encoding a Nonribosomal Peptide Synthetase Predicted To Produce the Ionophore Antibiotic Valinomycin. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
277	Role of cell surface composition and lysis in static biofilm formation by <i>Lactobacillus plantarum</i> WCFS1. <i>International Journal of Food Microbiology</i> , 2018, 271, 15-23.	4.7	11
278	Phenotypic and genetic characterization of differential galacto-oligosaccharide utilization in <i>Lactobacillus plantarum</i> . <i>Scientific Reports</i> , 2020, 10, 21657.	3.3	11
279	Host Genotype and the Effect on Microbial Communities. , 2011, , 15-41.		11
280	The structure of an alternative wall teichoic acid produced by a <i>Lactobacillus plantarum</i> WCFS1 mutant contains a 1,5-linked poly(ribitol phosphate) backbone with 2- α -D-glucosyl substitutions. <i>Carbohydrate Research</i> , 2013, 370, 67-71.	2.3	10
281	Laxative treatment with polyethylene glycol decreases microbial primary bile salt dehydroxylation and lipid metabolism in the intestine of rats. <i>American Journal of Physiology - Renal Physiology</i> , 2013, 305, G474-G482.	3.4	10
282	Molecular signatures for the dynamic process of establishing intestinal host – microbial homeostasis. <i>Current Opinion in Gastroenterology</i> , 2013, 29, 621-627.	2.3	10
283	Resequencing of the <i>Lactobacillus plantarum</i> Strain WJL Genome. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
284	TLR Signaling-induced CD103-expressing Cells Protect Against Intestinal Inflammation. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 507-519.	1.9	10
285	Heterologous Expression of the Pneumococcal Serotype 14 Polysaccharide in <i>Lactococcus lactis</i> Requires Lactococcal <i>epsABC</i> Regulatory Genes. <i>Applied and Environmental Microbiology</i> , 2008, 74, 912-915.	3.1	9
286	Functional analysis of the role of CggR (central glycolytic gene regulator) in <i>Lactobacillus plantarum</i> by transcriptome analysis. <i>Microbial Biotechnology</i> , 2011, 4, 345-356.	4.2	9
287	Complete Genome Sequence of <i>Streptococcus salivarius</i> HSISS4, a Human Commensal Bacterium Highly Prevalent in the Digestive Tract. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
288	Draft Genome Sequence of <i>Veillonella parvula</i> HSIVP1, Isolated from the Human Small Intestine. <i>Genome Announcements</i> , 2013, 1, .	0.8	8

#	ARTICLE	IF	CITATIONS
289	Biomarker Research in ADHD: the Impact of Nutrition (BRAIN) - study protocol of an open-label trial to investigate the mechanisms underlying the effects of a few-foods diet on ADHD symptoms in children. <i>BMJ Open</i> , 2019, 9, e029422.	1.9	8
290	Evaluating single-particle tracking by photo-activation localization microscopy (sptPALM) in <i>Lactococcus lactis</i> . <i>Physical Biology</i> , 2019, 16, 035001.	1.8	8
291	The Possible Link Between Manufacturing and Probiotic Efficacy; a Molecular Point of View on <i>Bifidobacterium</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 812536.	3.5	8
292	Lactic acid bacteria: life after genomics. <i>Microbial Biotechnology</i> , 2011, 4, 318-322.	4.2	7
293	Characterization of the pathophysiological determinants of diarrheagenic <i>Escherichia coli</i> infection using a challenge model in healthy adults. <i>Scientific Reports</i> , 2021, 11, 6060.	3.3	7
294	Dietary Inulin Increases <i>Lactiplantibacillus plantarum</i> Strain Lp900 Persistence in Rats Depending on the Dietary-Calcium Level. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	7
295	Microbial metabolic gatekeeping in the jejunum. <i>Nature Microbiology</i> , 2018, 3, 650-651.	13.3	6
296	Control of Folate Production in Lactic Acid Bacteria by Using Metabolic Engineering. , 2002, , 623-630.		6
297	The growth-survival trade-off is hard-wired in the <i>Lactococcus lactis</i> gene regulation network. <i>Environmental Microbiology Reports</i> , 2022, 14, 632-636.	2.4	6
298	The <i>qmeA</i> (ts) mutation of <i>Escherichia coli</i> is localized in the <i>fabI</i> gene, which encodes enoyl-ACP reductase. <i>Research in Microbiology</i> , 1996, 147, 609-613.	2.1	5
299	Engineering Robust Lactic Acid Bacteria. , 2011, , 369-394.		5
300	Colonizing Microbes, IL-10 and IL-22: Keeping the Peace at the Mucosal Surface. <i>Frontiers in Microbiology</i> , 2021, 12, 729053.	3.5	5
301	Correlation between brain function and ADHD symptom changes in children with ADHD following a few-foods diet: an open-label intervention trial. <i>Scientific Reports</i> , 2021, 11, 22205.	3.3	5
302	Large Intergenic Cruciform-Like Supermotifs in the <i>Lactobacillus plantarum</i> Genome. <i>Journal of Bacteriology</i> , 2009, 191, 3420-3423.	2.2	4
303	Characterization of the transcriptional regulation of the <i>tarIJKL</i> locus involved in ribitol-containing wall teichoic acid biosynthesis in <i>Lactobacillus plantarum</i> . <i>Microbiology (United Kingdom)</i> , 2016, 162, 420-432.	1.8	4
304	Microbial Functionality in the Human Gastrointestinal Tract. <i>Microbes and Environments</i> , 2004, 19, 276-280.	1.6	3
305	Draft Genome Sequence of <i>Enterococcus</i> sp. Strain HSIEG1, Isolated from the Human Small Intestine. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
306	KREAP: an automated Galaxy platform to quantify in vitro re-epithelialization kinetics. <i>GigaScience</i> , 2018, 7, .	6.4	3

#	ARTICLE	IF	CITATIONS
307	Using fluorescent promoter-reporters to study sugar utilization control in <i>Bifidobacterium longum</i> NCC 2705. <i>Scientific Reports</i> , 2022, 12, .	3.3	3
308	Molecular Analysis of Host-Microbe Interactions in the Gastrointestinal Tract. , 2006, , 169-187.		2
309	Draft Genome Sequence of <i>Lactobacillus plantarum</i> SF2A35B. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
310	A salivary metabolite signature that reflects gingival host-microbe interactions: instability predicts gingivitis susceptibility. <i>Scientific Reports</i> , 2020, 10, 3008.	3.3	2
311	Genetics of the Metabolism of Lactose and Other Sugars. , 2003, , 95-119.		2
312	Assessing the Impact of Diet on the Mucosa-Adhered Microbiome in Piglets Using Comparative Analysis of Rectal Swabs and Colon Content. <i>Frontiers in Microbiology</i> , 2022, 13, 804986.	3.5	2
313	Molecular advances and novel directions in food biotechnology innovation. <i>Current Opinion in Biotechnology</i> , 2006, 17, 179-182.	6.6	1
314	Complete Closed Genome Sequence of the Inulin-Utilizing <i>Lactiplantibacillus plantarum</i> Strain Lp900, Obtained Using a Hybrid Nanopore and Illumina Assembly. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
315	High-Throughput Screening Model to Quantify Re-Epithelialization Kinetics. <i>Protocol Exchange</i> , 0, , .	0.3	1
316	Improving the Digestive Tract Robustness of Probiotic <i>Lactobacilli</i> . , 2015, , 195-204.		1
317	Induction of Natural Competence in Genetically-modified <i>Lactococcus lactis</i> . <i>Bio-protocol</i> , 2018, 8, e2922.	0.4	1
318	Manganese Modulates Metabolic Activity and Redox Homeostasis in Translationally Blocked <i>Lactococcus cremoris</i> , Impacting Metabolic Persistence, Cell Culturability, and Flavor Formation. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	1
319	Predicting cis-acting elements of <i>Lactobacillus plantarum</i> by comparative genomics with different taxonomic subgroups. <i>Nucleic Acids Research</i> , 2006, 34, 2844-2844.	14.5	0
320	Post-genomic deciphering of host-microbe communication in the human intestine, and its clinical implications. <i>European Journal of Pharmacology</i> , 2011, 668, e1-e2.	3.5	0
321	P-015: Human buccal epithelium acquires microbial hyporesponsiveness at birth, a role for secretory leukocyte protease inhibitor. <i>Journal of Crohn's and Colitis</i> , 2014, 8, S398.	1.3	0
322	Editorial overview: Food biotechnology: Microbial ecosystem management: strategies to adapt ecosystems to improve performance and health impact. <i>Current Opinion in Biotechnology</i> , 2015, 32, v-viii.	6.6	0
323	Engineering <i>Lactococci</i> for Increased Functionality. , 2022, , 113-122.		0