

Michiel Kleerebezem

List of Publications by Year in descending order

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323
papers

51,676
citations

2423

97
h-index

1589

216
g-index

336
all docs

336
docs citations

336
times ranked

42676
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
2	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
3	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
4	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
5	Complete genome sequence of <i>Lactobacillus plantarum</i> WCFS1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1990-1995.	3.3	1,326
6	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
7	Quorum sensing by peptide pheromones and two-component signal-transduction systems in Gram-positive bacteria. <i>Molecular Microbiology</i> , 1997, 24, 895-904.	1.2	710
8	Quorum sensing-controlled gene expression in lactic acid bacteria. <i>Journal of Biotechnology</i> , 1998, 64, 15-21.	1.9	641
9	Emerging molecular insights into the interaction between probiotics and the host intestinal mucosa. <i>Nature Reviews Microbiology</i> , 2012, 10, 66-78.	13.6	557
10	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. <i>ISME Journal</i> , 2012, 6, 1415-1426.	4.4	544
11	Butyrate-producing <i>Clostridium</i> cluster XIVa species specifically colonize mucins in an <i>in vitro</i> gut model. <i>ISME Journal</i> , 2013, 7, 949-961.	4.4	501
12	10 years of the nisin-controlled gene expression system (NICE) in <i>Lactococcus lactis</i> . <i>Applied Microbiology and Biotechnology</i> , 2005, 68, 705-717.	1.7	498
13	Stress Physiology of Lactic Acid Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 837-890.	2.9	487
14	Regulation of human epithelial tight junction proteins by <i>Lactobacillus plantarum</i> <i>in vivo</i> and protective effects on the epithelial barrier. <i>American Journal of Physiology - Renal Physiology</i> , 2010, 298, G851-G859.	1.6	481
15	<i>Lactobacillus plantarum</i> survival, functional and potential probiotic properties in the human intestinal tract. <i>International Dairy Journal</i> , 2006, 16, 1018-1028.	1.5	410
16	Differential NF- κ B pathways induction by <i>Lactobacillus plantarum</i> in the duodenum of healthy humans correlating with immune tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2371-2376.	3.3	363
17	Can probiotics modulate human disease by impacting intestinal barrier function?. <i>British Journal of Nutrition</i> , 2017, 117, 93-107.	1.2	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. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 303, G589-G599.	1.6	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.	3.3	323
20	Microbiota conservation and BMI signatures in adult monozygotic twins. ISME Journal, 2013, 7, 707-717.	4.4	311
21	The extracellular biology of the lactobacilli. FEMS Microbiology Reviews, 2010, 34, 199-230.	3.9	304
22	Regulation of intestinal homeostasis and immunity with probiotic lactobacilli. Trends in Immunology, 2013, 34, 208-215.	2.9	294
23	Exopolysaccharides produced by lactic acid bacteria: from health-promoting benefits to stress tolerance mechanisms. Applied Microbiology and Biotechnology, 2016, 100, 3877-3886.	1.7	291
24	New insights in the molecular biology and physiology of revealed by comparative genomics. FEMS Microbiology Reviews, 2005, 29, 435-463.	3.9	289
25	Probiotic and Gut Lactobacilli and Bifidobacteria: Molecular Approaches to Study Diversity and Activity. Annual Review of Microbiology, 2009, 63, 269-290.	2.9	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.	3.3	289
27	Towards understanding molecular modes of probiotic action. Current Opinion in Biotechnology, 2006, 17, 204-210.	3.3	281
28	Biodiversity-Based Identification and Functional Characterization of the Mannose-Specific Adhesin of Lactobacillus plantarum. Journal of Bacteriology, 2005, 187, 6128-6136.	1.0	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.	1.4	272
30	Phenotypic and genomic diversity of <i>Lactobacillus plantarum</i> strains isolated from various environmental niches. Environmental Microbiology, 2010, 12, 758-773.	1.8	262
31	High temporal and inter-individual variation detected in the human ileal microbiota. Environmental Microbiology, 2010, 12, 3213-3227.	1.8	254
32	Towards microbial fermentation metabolites as markers for health benefits of prebiotics. Nutrition Research Reviews, 2015, 28, 42-66.	2.1	251
33	Cell to cell communication by autoinducing peptides in gram-positive bacteria. Antonie Van Leeuwenhoek, 2002, 81, 233-243.	0.7	248
34	The impact of probiotics and prebiotics on the immune system. Nature Reviews Immunology, 2012, 12, 728-734.	10.6	247
35	Improved Vectors for Nisin-Controlled Expression in Gram-Positive Bacteria. Plasmid, 2000, 44, 183-190.	0.4	244
36	Production of Aroma Compounds in Lactic Fermentations. Annual Review of Food Science and Technology, 2014, 5, 313-326.	5.1	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.	1.4	231
38	Exploring <i>Lactobacillus plantarum</i> Genome Diversity by Using Microarrays. <i>Journal of Bacteriology</i> , 2005, 187, 6119-6127.	1.0	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.	1.0	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.	1.8	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.	1.0	211
42	Controlled overproduction of proteins by lactic acid bacteria. <i>Trends in Biotechnology</i> , 1997, 15, 135-140.	4.9	208
43	Cre-lox -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.	1.4	207
44	Microbiome dynamics of human epidermis following skin barrier disruption. <i>Genome Biology</i> , 2012, 13, R101.	13.9	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.	2.7	201
46	Quorum sensing control of lantibiotic production; nisin and subtilin autoregulate their own biosynthesis. <i>Peptides</i> , 2004, 25, 1405-1414.	1.2	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.	1.8	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.	0.7	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.	1.5	182
50	The small intestine microbiota, nutritional modulation and relevance for health. <i>Current Opinion in Biotechnology</i> , 2015, 32, 14-20.	3.3	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.	1.2	179
52	Multifactorial diversity sustains microbial community stability. <i>ISME Journal</i> , 2013, 7, 2126-2136.	4.4	176
53	Conversion of <i>Lactococcus lactis</i> from homolactic to homoalanine fermentation through metabolic engineering. <i>Nature Biotechnology</i> , 1999, 17, 588-592.	9.4	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.	1.4	173

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55	The extracellular biology of the lactobacilli. FEMS Microbiology Reviews, 2010, 34, 199-230.	3.9	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.	3.5	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.	1.4	171
58	Isolation of DNA from bacterial samples of the human gastrointestinal tract. Nature Protocols, 2006, 1, 870-873.	5.5	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.	1.1	170
60	Increased Production of Folate by Metabolic Engineering of Lactococcus lactis. Applied and Environmental Microbiology, 2003, 69, 3069-3076.	1.4	169
61	Lactococcus lactis as a Cell Factory for High-Level Diacetyl Production. Applied and Environmental Microbiology, 2000, 66, 4112-4114.	1.4	168
62	Discovering lactic acid bacteria by genomics. Antonie Van Leeuwenhoek, 2002, 82, 29-58.	0.7	164
63	Identification of Lactobacillus plantarum genes modulating the cytokine response of human peripheral blood mononuclear cells. BMC Microbiology, 2010, 10, 293.	1.3	162
64	Comparative analysis of proteins with a mucus-binding domain found exclusively in lactic acid bacteria. Microbiology (United Kingdom), 2006, 152, 273-280.	0.7	155
65	Microbial domestication signatures of <i>Lactococcus lactis</i> can be reproduced by experimental evolution. Genome Research, 2012, 22, 115-124.	2.4	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.	1.4	150
67	Adaptation of the Nisin-Controlled Expression System in Lactobacillus plantarum : a Tool To Study In Vivo Biological Effects. Applied and Environmental Microbiology, 2000, 66, 4427-4432.	1.4	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.	1.0	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.	1.4	141
70	DNA micro-array-based identification of bile-responsive genes in Lactobacillus plantarum. Journal of Applied Microbiology, 2006, 100, 728-738.	1.4	139
71	Metabolic pathway engineering in lactic acid bacteria. Current Opinion in Biotechnology, 2003, 14, 232-237.	3.3	138
72	Microbiome and skin diseases. Current Opinion in Allergy and Clinical Immunology, 2013, 13, 514-520.	1.1	138

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73	Metabolic Engineering of Acetaldehyde Production by <i>Streptococcus thermophilus</i> . Applied and Environmental Microbiology, 2002, 68, 5656-5662.	1.4	134
74	Genome-Wide Detection and Analysis of Cell Wall-Bound Proteins with LPxTG-Like Sorting Motifs. Journal of Bacteriology, 2005, 187, 4928-4934.	1.0	134
75	On the ecosystemic network of saliva in healthy young adults. ISME Journal, 2017, 11, 1218-1231.	4.4	132
76	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. Microbiome, 2017, 5, 43.	4.9	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.	1.0	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.	1.4	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.	1.4	122
80	Diversity of human small intestinal <i>Streptococcus</i> and <i>Veillonella</i> populations. FEMS Microbiology Ecology, 2013, 85, 376-388.	1.3	121
81	The gut microbiota elicits a profound metabolic reorientation in the mouse jejunal mucosa during conventionalisation. Gut, 2013, 62, 1306-1314.	6.1	118
82	Immunomodulatory Properties of <i>Streptococcus</i> and <i>Veillonella</i> Isolates from the Human Small Intestine Microbiota. PLoS ONE, 2014, 9, e114277.	1.1	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.	1.5	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.	1.4	117
85	Microbial communities in the human small intestine: coupling diversity to metagenomics. Future Microbiology, 2007, 2, 285-295.	1.0	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.	1.0	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.	1.6	115
88	Metabolic engineering of lactic acid bacteria for the production of nutraceuticals. Antonie Van Leeuwenhoek, 2002, 82, 217-235.	0.7	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.	1.0	111
90	A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. BMC Genomics, 2013, 14, 530.	1.2	111

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91	The gut microbiota and mucosal homeostasis. <i>Gut Microbes</i> , 2013, 4, 118-124.	4.3	111
92	Complete Resequencing and Reannotation of the <i>Lactobacillus plantarum</i> WCFS1 Genome. <i>Journal of Bacteriology</i> , 2012, 194, 195-196.	1.0	109
93	High-Level Production of the Low-Calorie Sugar Sorbitol by <i>Lactobacillus plantarum</i> through Metabolic Engineering. <i>Applied and Environmental Microbiology</i> , 2007, 73, 1864-1872.	1.4	108
94	In vivo nuclear magnetic resonance studies of glycolytic kinetics in <i>Lactococcus lactis</i> . , 1999, 64, 200-212.		107
95	Spatial and Temporal Expression of <i>Lactobacillus plantarum</i> Genes in the Gastrointestinal Tracts of Mice. <i>Applied and Environmental Microbiology</i> , 2007, 73, 124-132.	1.4	107
96	Title is missing!. <i>Antonie Van Leeuwenhoek</i> , 1999, 76, 357-365.	0.7	105
97	Improvement of an experimental colitis in rats by lactic acid bacteria producing superoxide dismutase. <i>Inflammatory Bowel Diseases</i> , 2006, 12, 1044-1052.	0.9	104
98	The complete genomes of <i>Lactobacillus plantarum</i> and <i>Lactobacillus johnsonii</i> reveal extensive differences in chromosome organization and gene content. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3601-3611.	0.7	103
99	Strain-Specific Features of Extracellular Polysaccharides and Their Impact on <i>Lactobacillus plantarum</i> -Host Interactions. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3959-3970.	1.4	102
100	Functional Analysis of Three Plasmids from <i>Lactobacillus plantarum</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 1223-1230.	1.4	100
101	New insights in the molecular biology and physiology of <i>Streptococcus thermophilus</i> revealed by comparative genomics. <i>FEMS Microbiology Reviews</i> , 2005, 29, 435-463.	3.9	99
102	Lifestyle of <i>Lactobacillus plantarum</i> in the mouse caecum. <i>Environmental Microbiology</i> , 2009, 11, 2747-2757.	1.8	99
103	Dietary Heme Alters Microbiota and Mucosa of Mouse Colon without Functional Changes in Host-Microbe Cross-Talk. <i>PLoS ONE</i> , 2012, 7, e49868.	1.1	99
104	Involvement of stress protein PspA (phage shock protein A) of <i>Escherichia coli</i> in maintenance of the protonmotive force under stress conditions. <i>EMBO Journal</i> , 1996, 15, 162-71.	3.5	99
105	Metabolic engineering of lactic acid bacteria: overview of the approaches and results of pathway rerouting involved in food fermentations. <i>Current Opinion in Biotechnology</i> , 1999, 10, 492-497.	3.3	98
106	<i>Lactobacillus plantarum</i> gene clusters encoding putative cell-surface protein complexes for carbohydrate utilization are conserved in specific gram-positive bacteria. <i>BMC Genomics</i> , 2006, 7, 126.	1.2	96
107	Short- and Long-Term Adaptation to Ethanol Stress and Its Cross-Protective Consequences in <i>Lactobacillus plantarum</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 5247-5256.	1.4	96
108	Impact of 4 <i>Lactobacillus plantarum</i> capsular polysaccharide clusters on surface glycan composition and host cell signaling. <i>Microbial Cell Factories</i> , 2012, 11, 149.	1.9	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.	1.0	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.	0.7	95
111	Convergence in probiotic <i>Lactobacillus</i> gut-adaptive responses in humans and mice. <i>ISME Journal</i> , 2010, 4, 1481-1484.	4.4	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.	1.4	93
113	Functional implications of the microbial community structure of undefined mesophilic starter cultures. <i>Microbial Cell Factories</i> , 2014, 13, S2.	1.9	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.	3.3	92
115	Lactate racemase is a nickel-dependent enzyme activated by a widespread maturation system. <i>Nature Communications</i> , 2014, 5, 3615.	5.8	91
116	The quest for probiotic effector molecules—Unraveling strain specificity at the molecular level. <i>Pharmacological Research</i> , 2013, 69, 61-74.	3.1	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.	2.9	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.	1.4	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.	1.0	85
120	High-Level Acetaldehyde Production in <i>Lactococcus lactis</i> by Metabolic Engineering. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1109-1113.	1.4	84
121	Gut bacteria—host metabolic interplay during conventionalisation of the mouse germfree colon. <i>ISME Journal</i> , 2013, 7, 743-755.	4.4	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.	1.0	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.	1.4	82
124	Isolation of RNA from bacterial samples of the human gastrointestinal tract. <i>Nature Protocols</i> , 2006, 1, 954-959.	5.5	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.	2.0	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.	1.0	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.	1.6	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.	2.2	80
129	Expression of the <i>pspA</i> gene stimulates efficient protein export in <i>Escherichia coli</i> . Molecular Microbiology, 1993, 7, 947-956.	1.2	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.	1.0	79
131	Recombinant lactic acid bacteria as mucosal biotherapeutic agents. Trends in Biotechnology, 2011, 29, 499-508.	4.9	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.	1.4	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.	0.7	74
135	Evolutionary engineering to enhance starter culture performance in food fermentations. Current Opinion in Biotechnology, 2015, 32, 1-7.	3.3	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.	1.0	74
137	Visualisation of dCas9 target search in vivo using an open-microscopy framework. Nature Communications, 2019, 10, 3552.	5.8	70
138	Identification of the transcriptional response of human intestinal mucosa to <i>Lactobacillus plantarum</i> WCFS1 in vivo. BMC Genomics, 2008, 9, 374.	1.2	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.	1.0	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.	0.7	68
141	Potential and Opportunities for Use of Recombinant Lactic Acid Bacteria in Human Health. Advances in Applied Microbiology, 2004, 56, 1-64.	1.3	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.	1.0	66
143	<i>d</i> -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.	1.0	66
144	Cell surface-associated compounds of probiotic lactobacilli sustain the strain-specificity dogma. Current Opinion in Microbiology, 2013, 16, 262-269.	2.3	66

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145	The prophage sequences of <i>Lactobacillus plantarum</i> strain WCFS1. <i>Virology</i> , 2003, 316, 245-255.	1.1	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.	1.4	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.	1.0	64
148	Genome data mining of lactic acid bacteria: the impact of bioinformatics. <i>Current Opinion in Biotechnology</i> , 2004, 15, 105-115.	3.3	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.	1.0	61
150	Intestinal colonization: How key microbial players become established in this dynamic process. <i>BioEssays</i> , 2013, 35, 913-923.	1.2	61
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