

# Michiel Kleerebezem

## List of Publications by Year in descending order

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323  
papers

51,676  
citations

2427  
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336  
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336  
docs citations

336  
times ranked

42676  
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineering Lactococci for Increased Functionality. , 2022, , 113-122.		0
2	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
3	The growthâ€survival tradeâ€off is hardâ€wired in the <i>Lactococcus lactis</i> gene regulation network. <i>Environmental Microbiology Reports</i> , 2022, 14, 632-636.	2.4	6
4	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
5	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
6	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
7	Impact of early-life feeding on local intestinal microbiota and digestive system development in piglets. <i>Scientific Reports</i> , 2021, 11, 4213.	3.3	24
8	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
9	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
10	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
11	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
12	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
13	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
14	Dietary calcium phosphate strongly impacts gut microbiome changes elicited by inulin and galacto-oligosaccharides consumption. <i>Microbiome</i> , 2021, 9, 218.	11.1	32
15	Early life feeding accelerates gut microbiome maturation and suppresses acute postâ€weaning stress in piglets. <i>Environmental Microbiology</i> , 2021, 23, 7201-7213.	3.8	36
16	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
17	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
18	Lifestyle, metabolism and environmental adaptation in <i>Lactococcus lactis</i> . <i>FEMS Microbiology Reviews</i> , 2020, 44, 804-820.	8.6	29

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19	Synbiotic Matchmaking in <i>Lactobacillus plantarum</i> : Substrate Screening and Gene-Trait Matching To Characterize Strain-Specific Carbohydrate Utilization. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	23
20	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
21	Lipoproteins Contribute to the Anti-inflammatory Capacity of <i>Lactobacillus plantarum</i> WCFS1. <i>Frontiers in Microbiology</i> , 2020, 11, 1822.	3.5	13
22	Phenotypic and genetic characterization of differential galacto-oligosaccharide utilization in <i>Lactobacillus plantarum</i> . <i>Scientific Reports</i> , 2020, 10, 21657.	3.3	11
23	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
24	Intestinal Microbiota and Immune Modulation in Zebrafish by Fucoidan From Okinawa Mozuku ( <i>Cladosiphon okamuranus</i> ). <i>Frontiers in Nutrition</i> , 2020, 7, 67.	3.7	30
25	A salivary metabolite signature that reflects gingival host-microbe interactions: instability predicts gingivitis susceptibility. <i>Scientific Reports</i> , 2020, 10, 3008.	3.3	2
26	Visualisation of dCas9 target search in vivo using an open-microscopy framework. <i>Nature Communications</i> , 2019, 10, 3552.	12.8	70
27	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
28	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
29	Legitimate and Reliable Determination of the Age-Related Intestinal Microbiome in Young Piglets; Rectal Swabs and Fecal Samples Provide Comparable Insights. <i>Frontiers in Microbiology</i> , 2019, 10, 1886.	3.5	19
30	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
31	Sialyllactose and Galactooligosaccharides Promote Epithelial Barrier Functioning and Distinctly Modulate Microbiota Composition and Short Chain Fatty Acid Production In Vitro. <i>Frontiers in Immunology</i> , 2019, 10, 94.	4.8	80
32	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
33	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
34	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
35	Versatile Cas9-Driven Subpopulation Selection Toolbox for <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	43
36	Microbial metabolic gatekeeping in the jejunum. <i>Nature Microbiology</i> , 2018, 3, 650-651.	13.3	6

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37	Metatranscriptome analysis of the microbial fermentation of dietary milk proteins in the murine gut. PLoS ONE, 2018, 13, e0194066.	2.5	14
38	Dietary diversity affects feeding behaviour of suckling piglets. Applied Animal Behaviour Science, 2018, 205, 151-158.	1.9	24
39	KREAP: an automated Galaxy platform to quantify in vitro re-epithelialization kinetics. GigaScience, 2018, 7, .	6.4	3
40	Perspective: Fundamental Limitations of the Randomized Controlled Trial Method in Nutritional Research: The Example of Probiotics. Advances in Nutrition, 2018, 9, 561-571.	6.4	51
41	Lactic Acid Bacteria for Delivery of Endogenous or Engineered Therapeutic Molecules. Frontiers in Microbiology, 2018, 9, 1821.	3.5	31
42	Induction of Natural Competence in Genetically-modified Lactococcus lactis. Bio-protocol, 2018, 8, e2922.	0.4	1
43	Can probiotics modulate human disease by impacting intestinal barrier function?. British Journal of Nutrition, 2017, 117, 93-107.	2.3	343
44	On the ecosystemic network of saliva in healthy young adults. ISME Journal, 2017, 11, 1218-1231.	9.8	132
45	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. Microbiome, 2017, 5, 43.	11.1	132
46	Editorial: Lactic acid bacteriaâ€”a continuing journey in science and application. FEMS Microbiology Reviews, 2017, 41, S1-S2.	8.6	11
47	Streptococcus salivarius MS-oral-D6 promotes gingival re-epithelialization in vitro through a secreted serine protease. Scientific Reports, 2017, 7, 11100.	3.3	16
48	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
49	Unleashing Natural Competence in Lactococcus lactis by Induction of the Competence Regulator ComX. Applied and Environmental Microbiology, 2017, 83, .	3.1	25
50	Draft Genome Sequence of a Porcine Commensal, Rothia nasimurium, Encoding a Nonribosomal Peptide Synthetase Predicted To Produce the Ionophore Antibiotic Valinomycin. Genome Announcements, 2017, 5, .	0.8	11
51	Gram-positive anaerobe cocci are underrepresented in the microbiome of filaggrin-deficient human skin. Journal of Allergy and Clinical Immunology, 2017, 139, 1368-1371.	2.9	57
52	Reply to Meisel etÂal.. Journal of Investigative Dermatology, 2017, 137, 961-962.	0.7	43
53	The Variable Regions of <i>Lactobacillus rhamnosus</i> Genomes Reveal the Dynamic Evolution of Metabolic and Host-Adaptation Repertoires. Genome Biology and Evolution, 2016, 8, 1889-1905.	2.5	53
54	Draft Genome Sequence of Lactobacillus plantarum SF2A35B. Genome Announcements, 2016, 4, .	0.8	2

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55	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
56	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.	3.1	102
57	Stress Physiology of Lactic Acid Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 837-890.	6.6	487
58	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
59	Identification of Commensal Species Positively Correlated with Early Stress Responses to a Compromised Mucus Barrier. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 826-840.	1.9	30
60	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
61	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
62	Exopolysaccharides produced by lactic acid bacteria: from health-promoting benefits to stress tolerance mechanisms. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 3877-3886.	3.6	291
63	Characterization of the transcriptional regulation of the <i>tarJLKL</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
64	Functional Profiling of Unfamiliar Microbial Communities Using a Validated De Novo Assembly Metatranscriptome Pipeline. <i>PLoS ONE</i> , 2016, 11, e0146423.	2.5	23
65	Towards microbial fermentation metabolites as markers for health benefits of prebiotics. <i>Nutrition Research Reviews</i> , 2015, 28, 42-66.	4.1	251
66	Resequencing of the <i>Lactobacillus plantarum</i> Strain WJL Genome. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
67	Nearly Complete Genome Sequence of <i>Lactobacillus plantarum</i> Strain NIZO2877. <i>Genome Announcements</i> , 2015, 3, .	0.8	12
68	Physiological and cell morphology adaptation of <i>Bacillus subtilis</i> at near-zero specific growth rates: a transcriptome analysis. <i>Environmental Microbiology</i> , 2015, 17, 346-363.	3.8	26
69	Genome-Wide Transcriptional Responses to Carbon Starvation in Nongrowing <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 2554-2561.	3.1	19
70	Physiological and Transcriptional Responses of Different Industrial Microbes at Near-Zero Specific Growth Rates. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5662-5670.	3.1	42
71	Gut microbiota facilitates dietary heme-induced epithelial hyperproliferation by opening the mucus barrier in colon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10038-10043.	7.1	323
72	Mining microbial metatranscriptomes for expression of antibiotic resistance genes under natural conditions. <i>Scientific Reports</i> , 2015, 5, 11981.	3.3	50

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73	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
74	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
75	Comparison of the effects of five dietary fibers on mucosal transcriptional profiles, and luminal microbiota composition and SCFA concentrations in murine colon. <i>Molecular Nutrition and Food Research</i> , 2015, 59, 1590-1602.	3.3	41
76	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
77	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
78	TLR Signaling-induced CD103-expressing Cells Protect Against Intestinal Inflammation. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 507-519.	1.9	10
79	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
80	Evolutionary engineering to enhance starter culture performance in food fermentations. <i>Current Opinion in Biotechnology</i> , 2015, 32, 1-7.	6.6	74
81	The small intestine microbiota, nutritional modulation and relevance for health. <i>Current Opinion in Biotechnology</i> , 2015, 32, 14-20.	6.6	182
82	Improving the Digestive Tract Robustness of Probiotic <i>Lactobacilli</i> . , 2015, , 195-204.		1
83	Immunomodulatory Properties of <i>Streptococcus</i> and <i>Veillonella</i> Isolates from the Human Small Intestine Microbiota. <i>PLoS ONE</i> , 2014, 9, e114277.	2.5	118
84	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
85	Functional implications of the microbial community structure of undefined mesophilic starter cultures. <i>Microbial Cell Factories</i> , 2014, 13, S2.	4.0	93
86	H <sub>2</sub> O <sub>2</sub> Production in Species of the <i>Lactobacillus acidophilus</i> Group: a Central Role for a Novel NADH-Dependent Flavin Reductase. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2229-2239.	3.1	130
87	GtfA and GtfB Are Both Required for Protein <i>O</i> -Glycosylation in <i>Lactobacillus plantarum</i> . <i>Journal of Bacteriology</i> , 2014, 196, 1671-1682.	2.2	20
88	Lactate racemase is a nickel-dependent enzyme activated by a widespread maturation system. <i>Nature Communications</i> , 2014, 5, 3615.	12.8	91
89	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
90	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

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91	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	17.5	909
92	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	17.5	1,664
93	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
94	Production of Aroma Compounds in Lactic Fermentations. <i>Annual Review of Food Science and Technology</i> , 2014, 5, 313-326.	9.9	237
95	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
96	The gut microbiota elicits a profound metabolic reorientation in the mouse jejunal mucosa during conventionalisation. <i>Gut</i> , 2013, 62, 1306-1314.	12.1	118
97	Multifactorial diversity sustains microbial community stability. <i>ISME Journal</i> , 2013, 7, 2126-2136.	9.8	176
98	Omics approaches to study host-microbiota interactions. <i>Current Opinion in Microbiology</i> , 2013, 16, 270-277.	5.1	22
99	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	27.8	3,641
100	Intestinal colonization: How key microbial players become established in this dynamic process. <i>BioEssays</i> , 2013, 35, 913-923.	2.5	61
101	Cell surface-associated compounds of probiotic lactobacilli sustain the strain-specificity dogma. <i>Current Opinion in Microbiology</i> , 2013, 16, 262-269.	5.1	66
102	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- $\alpha$ -D-glucosyl substitutions. <i>Carbohydrate Research</i> , 2013, 370, 67-71.	2.3	10
103	A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. <i>BMC Genomics</i> , 2013, 14, 530.	2.8	111
104	Transcriptome signatures of class I and III stress response deregulation in <i>Lactobacillus plantarum</i> reveal pleiotropic adaptation. <i>Microbial Cell Factories</i> , 2013, 12, 112.	4.0	21
105	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
106	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
107	The quest for probiotic effector molecules—Unraveling strain specificity at the molecular level. <i>Pharmacological Research</i> , 2013, 69, 61-74.	7.1	88
108	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



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109	Quantitative physiology of <i>Lactococcus lactis</i> at extreme low growth rates. Environmental Microbiology, 2013, 15, 2319-2332.	3.8	18
110	Gut bacteria-host metabolic interplay during conventionalisation of the mouse germfree colon. ISME Journal, 2013, 7, 743-755.	9.8	84
111	Regulation of intestinal homeostasis and immunity with probiotic lactobacilli. Trends in Immunology, 2013, 34, 208-215.	6.8	294
112	Diversity of human small intestinal <i>Streptococcus</i> and <i>Veillonella</i> populations. FEMS Microbiology Ecology, 2013, 85, 376-388.	2.7	121
113	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
114	Influence of fermented milk products, prebiotics and probiotics on microbiota composition and health. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2013, 27, 139-155.	2.4	83
115	Draft Genome Sequence of <i>Veillonella parvula</i> HSIVP1, Isolated from the Human Small Intestine. Genome Announcements, 2013, 1, .	0.8	8
116	Draft Genome Sequence of <i>Enterococcus</i> sp. Strain HSIEG1, Isolated from the Human Small Intestine. Genome Announcements, 2013, 1, .	0.8	3
117	Microbiota conservation and BMI signatures in adult monozygotic twins. ISME Journal, 2013, 7, 707-717.	9.8	311
118	Laxative treatment with polyethylene glycol decreases microbial primary bile salt dehydroxylation and lipid metabolism in the intestine of rats. American Journal of Physiology - Renal Physiology, 2013, 305, G474-G482.	3.4	10
119	The gut microbiota and mucosal homeostasis. Gut Microbes, 2013, 4, 118-124.	9.8	111
120	Molecular signatures for the dynamic process of establishing intestinal host-microbial homeostasis. Current Opinion in Gastroenterology, 2013, 29, 621-627.	2.3	10
121	Microbiome and skin diseases. Current Opinion in Allergy and Clinical Immunology, 2013, 13, 514-520.	2.3	138
122	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
123	O-Glycosylation as a Novel Control Mechanism of Peptidoglycan Hydrolase Activity. Journal of Biological Chemistry, 2013, 288, 22233-22247.	3.4	42
124	Oxygen Relieves the CO <sub>2</sub> and Acetate Dependency of <i>Lactobacillus johnsonii</i> NCC 533. PLoS ONE, 2013, 8, e57235.	2.5	20
125	Comparative Genomics Analysis of <i>Streptococcus</i> Isolates from the Human Small Intestine Reveals their Adaptation to a Highly Dynamic Ecosystem. PLoS ONE, 2013, 8, e83418.	2.5	57
126	The Impact of <i>Lactobacillus plantarum</i> WCFS1 Teichoic Acid D-Alanylation on the Generation of Effector and Regulatory T-cells in Healthy Mice. PLoS ONE, 2013, 8, e63099.	2.5	47



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127	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
128	Microbial domestication signatures of <i>Lactococcus lactis</i> can be reproduced by experimental evolution. <i>Genome Research</i> , 2012, 22, 115-124.	5.5	154
129	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
130	Complete Resequencing and Reannotation of the <i>Lactobacillus plantarum</i> WCFS1 Genome. <i>Journal of Bacteriology</i> , 2012, 194, 195-196.	2.2	109
131	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.	3.4	330
132	Comparative Analysis of <i>Lactobacillus plantarum</i> WCFS1 Transcriptomes by Using DNA Microarray and Next-Generation Sequencing Technologies. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4141-4148.	3.1	24
133	Genome-Wide Prediction and Validation of Sigma70 Promoters in <i>Lactobacillus plantarum</i> WCFS1. <i>PLoS ONE</i> , 2012, 7, e45097.	2.5	13
134	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. <i>ISME Journal</i> , 2012, 6, 1415-1426.	9.8	544
135	Novel Method for Enumeration of Viable <i>Lactobacillus plantarum</i> WCFS1 Cells after Single-Droplet Drying. <i>Applied and Environmental Microbiology</i> , 2012, 78, 8082-8088.	3.1	24
136	Microbiome dynamics of human epidermis following skin barrier disruption. <i>Genome Biology</i> , 2012, 13, R101.	9.6	201
137	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
138	Toward pectin fermentation by <i>Saccharomyces cerevisiae</i> : Expression of the first two steps of a bacterial pathway for d-galacturonate metabolism. <i>Journal of Biotechnology</i> , 2012, 162, 303-310.	3.8	26
139	<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
140	Identification of key peptidoglycan hydrolases for morphogenesis, autolysis, and peptidoglycan composition of <i>Lactobacillus plantarum</i> WCFS1. <i>Microbial Cell Factories</i> , 2012, 11, 137.	4.0	45
141	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.	4.0	96
142	The impact of probiotics and prebiotics on the immune system. <i>Nature Reviews Immunology</i> , 2012, 12, 728-734.	22.7	247
143	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
144	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

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145	Emerging molecular insights into the interaction between probiotics and the host intestinal mucosa. Nature Reviews Microbiology, 2012, 10, 66-78.	28.6	557
146	Modulation of Lactobacillus plantarum Gastrointestinal Robustness by Fermentation Conditions Enables Identification of Bacterial Robustness Markers. PLoS ONE, 2012, 7, e39053.	2.5	56
147	Congruent Strain Specific Intestinal Persistence of Lactobacillus plantarum in an Intestine-Mimicking In Vitro System and in Human Volunteers. PLoS ONE, 2012, 7, e44588.	2.5	31
148	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
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