

Michiel Kleerebezem

List of Publications by Year in Descending Order

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Version: 2024-04-19

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

316
papers

39,702
citations

89
h-index

195
g-index

336
ext. papers

46,821
ext. citations

7
avg, IF

6.96
L-index

#	Paper	IF	Citations
316	Engineering Lactococci for Increased Functionality 2022 , 113-122		
315	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	5.7	
314	Dietary calcium phosphate strongly impacts gut microbiome changes elicited by inulin and galacto-oligosaccharides consumption. <i>Microbiome</i> , 2021 , 9, 218	16.6	2
313	Early life feeding accelerates gut microbiome maturation and suppresses acute post-weaning stress in piglets. <i>Environmental Microbiology</i> , 2021 , 23, 7201-7213	5.2	4
312	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	4.9	0
311	Carbohydrate-controlled serine protease inhibitor (serpin) production in <i>Bifidobacterium longum</i> subsp. <i>longum</i> . <i>Scientific Reports</i> , 2021 , 11, 7236	4.9	5
310	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	4.9	1
309	Dietary Inulin Increases Strain Lp900 Persistence in Rats Depending on the Dietary-Calcium Level. <i>Applied and Environmental Microbiology</i> , 2021 , 87,	4.8	4
308	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	9.8	4
307	Impact of early-life feeding on local intestinal microbiota and digestive system development in piglets. <i>Scientific Reports</i> , 2021 , 11, 4213	4.9	8
306	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	16.4	15
305	Colonizing Microbes, IL-10 and IL-22: Keeping the Peace at the Mucosal Surface. <i>Frontiers in Microbiology</i> , 2021 , 12, 729053	5.7	1
304	The Possible Link Between Manufacturing and Probiotic Efficacy; a Molecular Point of View on .. <i>Frontiers in Microbiology</i> , 2021 , 12, 812536	5.7	2
303	Effects of Creep Feed Provision on Behavior and Performance of Piglets Around Weaning. <i>Frontiers in Veterinary Science</i> , 2020 , 7, 520035	3.1	4
302	Intestinal Microbiota and Immune Modulation in Zebrafish by Fucoïdan From Okinawa Mozuku (). <i>Frontiers in Nutrition</i> , 2020 , 7, 67	6.2	12
301	A salivary metabolite signature that reflects gingival host-microbe interactions: instability predicts gingivitis susceptibility. <i>Scientific Reports</i> , 2020 , 10, 3008	4.9	
300	Lifestyle, metabolism and environmental adaptation in <i>Lactococcus lactis</i> . <i>FEMS Microbiology Reviews</i> , 2020 , 44, 804-820	15.1	4

299	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,	4.8	6
298	A Novel Method for Long-Term Analysis of Lactic Acid and Ammonium Production in Non-growing Reveals Pre-culture and Strain Dependence. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 580050	5.8	6
297	Lipoproteins Contribute to the Anti-inflammatory Capacity of WCFS1. <i>Frontiers in Microbiology</i> , 2020 , 11, 1822	5.7	5
296	Phenotypic and genetic characterization of differential galacto-oligosaccharide utilization in <i>Lactobacillus plantarum</i> . <i>Scientific Reports</i> , 2020 , 10, 21657	4.9	6
295	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	5.7	8
294	Evaluating single-particle tracking by photo-activation localization microscopy (sptPALM) in <i>Lactococcus lactis</i> . <i>Physical Biology</i> , 2019 , 16, 035001	3	5
293	Sialyllactose and Galactooligosaccharides Promote Epithelial Barrier Functioning and Distinctly Modulate Microbiota Composition and Short Chain Fatty Acid Production. <i>Frontiers in Immunology</i> , 2019 , 10, 94	8.4	53
292	Visualisation of dCas9 target search in vivo using an open-microscopy framework. <i>Nature Communications</i> , 2019 , 10, 3552	17.4	33
291	Microbial communities in a dynamic in vitro model for the human ileum resemble the human ileal microbiota. <i>FEMS Microbiology Ecology</i> , 2019 , 95,	4.3	6
290	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	3	6
289	Renaissance of traditional DNA transfer strategies for improvement of industrial lactic acid bacteria. <i>Current Opinion in Biotechnology</i> , 2019 , 56, 61-68	11.4	26
288	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	11.4	34
287	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	5.8	4
286	Versatile Cas9-Driven Subpopulation Selection Toolbox for <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	33
285	Dietary diversity affects feeding behaviour of suckling piglets. <i>Applied Animal Behaviour Science</i> , 2018 , 205, 151-158	2.2	13
284	KREAP: an automated Galaxy platform to quantify in vitro re-epithelialization kinetics. <i>GigaScience</i> , 2018 , 7,	7.6	3
283	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	10	33
282	Lactic Acid Bacteria for Delivery of Endogenous or Engineered Therapeutic Molecules. <i>Frontiers in Microbiology</i> , 2018 , 9, 1821	5.7	24

281	Induction of Natural Competence in Genetically-modified. <i>Bio-protocol</i> , 2018 , 8, e2922	0.9	1
280	Microbial metabolic gatekeeping in the jejunum. <i>Nature Microbiology</i> , 2018 , 3, 650-651	26.6	5
279	Metatranscriptome analysis of the microbial fermentation of dietary milk proteins in the murine gut. <i>PLoS ONE</i> , 2018 , 13, e0194066	3.7	9
278	Can probiotics modulate human disease by impacting intestinal barrier function?. <i>British Journal of Nutrition</i> , 2017 , 117, 93-107	3.6	218
277	On the ecosystemic network of saliva in healthy young adults. <i>ISME Journal</i> , 2017 , 11, 1218-1231	11.9	78
276	High-fat feeding rather than obesity drives taxonomical and functional changes in the gut microbiota in mice. <i>Microbiome</i> , 2017 , 5, 43	16.6	77
275	Streptococcus salivarius MS-oral-D6 promotes gingival re-epithelialization in vitro through a secreted serine protease. <i>Scientific Reports</i> , 2017 , 7, 11100	4.9	9
274	Intestinal colonisation patterns in breastfed and formula-fed infants during the first 12 weeks of life reveal sequential microbiota signatures. <i>Scientific Reports</i> , 2017 , 7, 8327	4.9	74
273	Unleashing Natural Competence in <i>Lactococcus lactis</i> by Induction of the Competence Regulator ComX. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	19
272	Draft Genome Sequence of a Porcine Commensal, , Encoding a Nonribosomal Peptide Synthetase Predicted To Produce the Ionophore Antibiotic Valinomycin. <i>Genome Announcements</i> , 2017 , 5,		7
271	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	11.5	36
270	Reply to Meisel et al. <i>Journal of Investigative Dermatology</i> , 2017 , 137, 961-962	4.3	29
269	Stress Physiology of Lactic Acid Bacteria. <i>Microbiology and Molecular Biology Reviews</i> , 2016 , 80, 837-90	13.2	276
268	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	5.2	106
267	Identification of Commensal Species Positively Correlated with Early Stress Responses to a Compromised Mucus Barrier. <i>Inflammatory Bowel Diseases</i> , 2016 , 22, 826-40	4.5	21
266	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, E886-99	6	34
265	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,		6
264	Exopolysaccharides produced by lactic acid bacteria: from health-promoting benefits to stress tolerance mechanisms. <i>Applied Microbiology and Biotechnology</i> , 2016 , 100, 3877-86	5.7	206

263	Functional Profiling of Unfamiliar Microbial Communities Using a Validated De Novo Assembly Metatranscriptome Pipeline. <i>PLoS ONE</i> , 2016 , 11, e0146423	3.7	16
262	Characterization of the transcriptional regulation of the tarIJKL locus involved in ribitol-containing wall teichoic acid biosynthesis in <i>Lactobacillus plantarum</i> . <i>Microbiology (United Kingdom)</i> , 2016 , 162, 420-432	2.9	4
261	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, 1889-905	3.9	39
260	Draft Genome Sequence of <i>Lactobacillus plantarum</i> SF2A35B. <i>Genome Announcements</i> , 2016 , 4,		2
259	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	5.8	34
258	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	4.8	73
257	Genome-wide transcriptional responses to carbon starvation in nongrowing <i>Lactococcus lactis</i> . <i>Applied and Environmental Microbiology</i> , 2015 , 81, 2554-61	4.8	16
256	Physiological and Transcriptional Responses of Different Industrial Microbes at Near-Zero Specific Growth Rates. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 5662-70	4.8	29
255	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, 10038-43	11.5	206
254	Mining microbial metatranscriptomes for expression of antibiotic resistance genes under natural conditions. <i>Scientific Reports</i> , 2015 , 5, 11981	4.9	41
253	Correlation of <i>Lactobacillus rhamnosus</i> Genotypes and Carbohydrate Utilization Signatures Determined by Phenotype Profiling. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 5458-70	4.8	29
252	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, 1590-602	5.9	29
251	Human buccal epithelium acquires microbial hyporesponsiveness at birth, a role for secretory leukocyte protease inhibitor. <i>Gut</i> , 2015 , 64, 884-93	19.2	12
250	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, 531-42	4.5	38
249	TLR signaling-induced CD103-expressing cells protect against intestinal inflammation. <i>Inflammatory Bowel Diseases</i> , 2015 , 21, 507-19	4.5	9
248	Molecular and metabolic adaptations of <i>Lactococcus lactis</i> at near-zero growth rates. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 320-31	4.8	15
247	Evolutionary engineering to enhance starter culture performance in food fermentations. <i>Current Opinion in Biotechnology</i> , 2015 , 32, 1-7	11.4	51
246	The small intestine microbiota, nutritional modulation and relevance for health. <i>Current Opinion in Biotechnology</i> , 2015 , 32, 14-20	11.4	130

245	Towards microbial fermentation metabolites as markers for health benefits of prebiotics. <i>Nutrition Research Reviews</i> , 2015 , 28, 42-66	7	173
244	Resequencing of the <i>Lactobacillus plantarum</i> Strain WJL Genome. <i>Genome Announcements</i> , 2015 , 3,		8
243	Nearly Complete Genome Sequence of <i>Lactobacillus plantarum</i> Strain NIZO2877. <i>Genome Announcements</i> , 2015 , 3,		7
242	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, 346-63	5.2	21
241	H ₂ O ₂ 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, 2229-39	4.8	91
240	GtfA and GtfB are both required for protein O-glycosylation in <i>Lactobacillus plantarum</i> . <i>Journal of Bacteriology</i> , 2014 , 196, 1671-82	3.5	17
239	Lactate racemase is a nickel-dependent enzyme activated by a widespread maturation system. <i>Nature Communications</i> , 2014 , 5, 3615	17.4	72
238	Development of the recombinase-based in vivo expression technology in <i>Streptococcus thermophilus</i> and validation using the lactose operon promoter. <i>Journal of Applied Microbiology</i> , 2014 , 116, 620-31	4.7	10
237	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	1.5	
236	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014 , 32, 822-8	44.5	624
235	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014 , 32, 834-41	44.5	1088
234	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	7	13
233	Production of aroma compounds in lactic fermentations. <i>Annual Review of Food Science and Technology</i> , 2014 , 5, 313-26	14.7	164
232	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	4.9	54
231	Immunomodulatory properties of <i>Streptococcus</i> and <i>Veillonella</i> isolates from the human small intestine microbiota. <i>PLoS ONE</i> , 2014 , 9, e114277	3.7	73
230	T lymphocytes control microbial composition by regulating the abundance of <i>Vibrio</i> in the zebrafish gut. <i>Gut Microbes</i> , 2014 , 5, 737-47	8.8	26
229	Functional implications of the microbial community structure of undefined mesophilic starter cultures. <i>Microbial Cell Factories</i> , 2014 , 13 Suppl 1, S2	6.4	55
228	The gut microbiota elicits a profound metabolic reorientation in the mouse jejunal mucosa during conventionalisation. <i>Gut</i> , 2013 , 62, 1306-14	19.2	88

227	Multifactorial diversity sustains microbial community stability. <i>ISME Journal</i> , 2013 , 7, 2126-36	11.9	113
226	Omics approaches to study host-microbiota interactions. <i>Current Opinion in Microbiology</i> , 2013 , 16, 270-7.9		22
225	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013 , 500, 541-6	50.4	2584
224	Intestinal colonization: how key microbial players become established in this dynamic process: microbial metabolic activities and the interplay between the host and microbes. <i>BioEssays</i> , 2013 , 35, 913-23	4.1	47
223	Cell surface-associated compounds of probiotic lactobacilli sustain the strain-specificity dogma. <i>Current Opinion in Microbiology</i> , 2013 , 16, 262-9	7.9	55
222	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- β -D-glucosyl substitutions. <i>Carbohydrate Research</i> , 2013 , 370, 67-71	2.9	8
221	A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. <i>BMC Genomics</i> , 2013 , 14, 530	4.5	92
220	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	6.4	15
219	Modulation of the microbial fermentation in the gut by fermentable carbohydrates. <i>Bioactive Carbohydrates and Dietary Fibre</i> , 2013 , 2, 133-142	3.4	19
218	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, 502-9	3.5	33
217	The quest for probiotic effector molecules--unraveling strain specificity at the molecular level. <i>Pharmacological Research</i> , 2013 , 69, 61-74	10.2	72
216	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	7	68
215	Quantitative physiology of <i>Lactococcus lactis</i> at extreme low-growth rates. <i>Environmental Microbiology</i> , 2013 , 15, 2319-32	5.2	14
214	Gut bacteria-host metabolic interplay during conventionalisation of the mouse germfree colon. <i>ISME Journal</i> , 2013 , 7, 743-55	11.9	73
213	Regulation of intestinal homeostasis and immunity with probiotic lactobacilli. <i>Trends in Immunology</i> , 2013 , 34, 208-15	14.4	222
212	Diversity of human small intestinal <i>Streptococcus</i> and <i>Veillonella</i> populations. <i>FEMS Microbiology Ecology</i> , 2013 , 85, 376-88	4.3	90
211	Butyrate-producing <i>Clostridium</i> cluster XIVa species specifically colonize mucins in an in vitro gut model. <i>ISME Journal</i> , 2013 , 7, 949-61	11.9	351
210	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, 139-55	2.5	64

209	Draft Genome Sequence of <i>Veillonella parvula</i> HSIVP1, Isolated from the Human Small Intestine. <i>Genome Announcements</i> , 2013 , 1,		7
208	Draft Genome Sequence of <i>Enterococcus</i> sp. Strain HSIEG1, Isolated from the Human Small Intestine. <i>Genome Announcements</i> , 2013 , 1,		3
207	Microbiota conservation and BMI signatures in adult monozygotic twins. <i>ISME Journal</i> , 2013 , 7, 707-17	11.9	221
206	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, G474-82	5.1	8
205	The gut microbiota and mucosal homeostasis: colonized at birth or at adulthood, does it matter?. <i>Gut Microbes</i> , 2013 , 4, 118-24	8.8	80
204	Molecular signatures for the dynamic process of establishing intestinal host-microbial homeostasis: potential for disease diagnostics?. <i>Current Opinion in Gastroenterology</i> , 2013 , 29, 621-7	3	8
203	Microbiome and skin diseases. <i>Current Opinion in Allergy and Clinical Immunology</i> , 2013 , 13, 514-20	3.3	104
202	Genotypic adaptations associated with prolonged persistence of <i>Lactobacillus plantarum</i> in the murine digestive tract. <i>Biotechnology Journal</i> , 2013 , 8, 895-904	5.6	15
201	O-glycosylation as a novel control mechanism of peptidoglycan hydrolase activity. <i>Journal of Biological Chemistry</i> , 2013 , 288, 22233-47	5.4	31
200	Oxygen relieves the CO ₂ and acetate dependency of <i>Lactobacillus johnsonii</i> NCC 533. <i>PLoS ONE</i> , 2013 , 8, e57235	3.7	18
199	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	3.7	42
198	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	3.7	37
197	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. <i>ISME Journal</i> , 2012 , 6, 1415-26	11.9	416
196	Novel method for enumeration of viable <i>Lactobacillus plantarum</i> WCFS1 cells after single-droplet drying. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 8082-8	4.8	21
195	Microbiome dynamics of human epidermis following skin barrier disruption. <i>Genome Biology</i> , 2012 , 13, R101	18.3	153
194	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, 251-9	4.9	48
193	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, 303-10	3.7	23
192	<i>Lactobacillus plantarum</i> possesses the capability for wall teichoic acid backbone alditol switching. <i>Microbial Cell Factories</i> , 2012 , 11, 123	6.4	41

191	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	6.4	35
190	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	6.4	74
189	The impact of probiotics and prebiotics on the immune system. <i>Nature Reviews Immunology</i> , 2012 , 12, 728-34	36.5	170
188	Transcriptomes reveal genetic signatures underlying physiological variations imposed by different fermentation conditions in <i>Lactobacillus plantarum</i> . <i>PLoS ONE</i> , 2012 , 7, e38720	3.7	43
187	Temporal and spatial interplay of microbiota and intestinal mucosa drive establishment of immune homeostasis in conventionalized mice. <i>Mucosal Immunology</i> , 2012 , 5, 567-79	9.2	152
186	The major autolysin Acm2 from <i>Lactobacillus plantarum</i> undergoes cytoplasmic O-glycosylation. <i>Journal of Bacteriology</i> , 2012 , 194, 325-33	3.5	36
185	Microbial domestication signatures of <i>Lactococcus lactis</i> can be reproduced by experimental evolution. <i>Genome Research</i> , 2012 , 22, 115-24	9.7	116
184	Genome sequence of the naturally plasmid-free <i>Lactobacillus plantarum</i> strain NC8 (CCUG 61730). <i>Journal of Bacteriology</i> , 2012 , 194, 2391-2	3.5	43
183	Complete resequencing and reannotation of the <i>Lactobacillus plantarum</i> WCFS1 genome. <i>Journal of Bacteriology</i> , 2012 , 194, 195-6	3.5	92
182	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, G589-99	5.1	250
181	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, 4141-8	4.8	24
180	Genome-wide prediction and validation of sigma70 promoters in <i>Lactobacillus plantarum</i> WCFS1. <i>PLoS ONE</i> , 2012 , 7, e45097	3.7	8
179	Modulation of <i>Lactobacillus plantarum</i> gastrointestinal robustness by fermentation conditions enables identification of bacterial robustness markers. <i>PLoS ONE</i> , 2012 , 7, e39053	3.7	44
178	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	3.7	29
177	Dietary heme alters microbiota and mucosa of mouse colon without functional changes in host-microbe cross-talk. <i>PLoS ONE</i> , 2012 , 7, e49868	3.7	79
176	Emerging molecular insights into the interaction between probiotics and the host intestinal mucosa. <i>Nature Reviews Microbiology</i> , 2011 , 10, 66-78	22.2	429
175	Functional Intestinal Metagenomics 2011 , 175-190		6
174	Fluorescence and atomic force microscopy imaging of wall teichoic acids in <i>Lactobacillus plantarum</i> . <i>ACS Chemical Biology</i> , 2011 , 6, 366-76	4.9	67

173	Human mucosal in vivo transcriptome responses to three lactobacilli indicate how probiotics may modulate human cellular pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108 Suppl 1, 4562-9	11.5	239
172	Arabinoxylans and inulin differentially modulate the mucosal and luminal gut microbiota and mucin-degradation in humanized rats. <i>Environmental Microbiology</i> , 2011 , 13, 2667-80	5.2	183
171	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, 232-42	4.1	33
170	<i>Lactobacillus</i> strains differentially modulate cytokine production by hPBMC from pollen-allergic patients. <i>FEMS Immunology and Medical Microbiology</i> , 2011 , 61, 28-40		21
169	High local substrate availability stabilizes a cooperative trait. <i>ISME Journal</i> , 2011 , 5, 929-32	11.9	35
168	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
167	Reconstruction of the regulatory network of <i>Lactobacillus plantarum</i> WCFS1 on basis of correlated gene expression and conserved regulatory motifs. <i>Microbial Biotechnology</i> , 2011 , 4, 333-44	6.3	18
166	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, 345-56	6.3	6
165	The human gut microbiome: are we our enterotypes?. <i>Microbial Biotechnology</i> , 2011 , 4, 550-3	6.3	42
164	Recombinant lactic acid bacteria as mucosal biotherapeutic agents. <i>Trends in Biotechnology</i> , 2011 , 29, 499-508	15.1	71
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10	Expression systems for industrial Gram-positive bacteria with low guanine and cytosine content. <i>Current Opinion in Biotechnology</i> , 1997 , 8, 547-53	11.4	41
9	Quorum sensing by peptide pheromones and two-component signal-transduction systems in Gram-positive bacteria. <i>Molecular Microbiology</i> , 1997 , 24, 895-904	4.1	607
8	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, 4581-4	4.8	196
7	The qmeA (ts) mutation of <i>Escherichia coli</i> is localized in the fabI gene, which encodes enoyl-ACP reductase. <i>Research in Microbiology</i> , 1996 , 147, 609-13	4	3
6	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, 162-171	13	151
5	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	13	89
4	Characterization of an <i>Escherichia coli</i> rotA mutant, affected in periplasmic peptidyl-prolyl cis/trans isomerase. <i>Molecular Microbiology</i> , 1995 , 18, 313-20	4.1	40
3	Expression of the pspA gene stimulates efficient protein export in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1993 , 7, 947-56	4.1	69
2	Early-life feeding accelerates gut microbiome maturation in piglets		2
1	An open microscopy framework suited for tracking dCas9 in live bacteria		5